

Fig. 1A

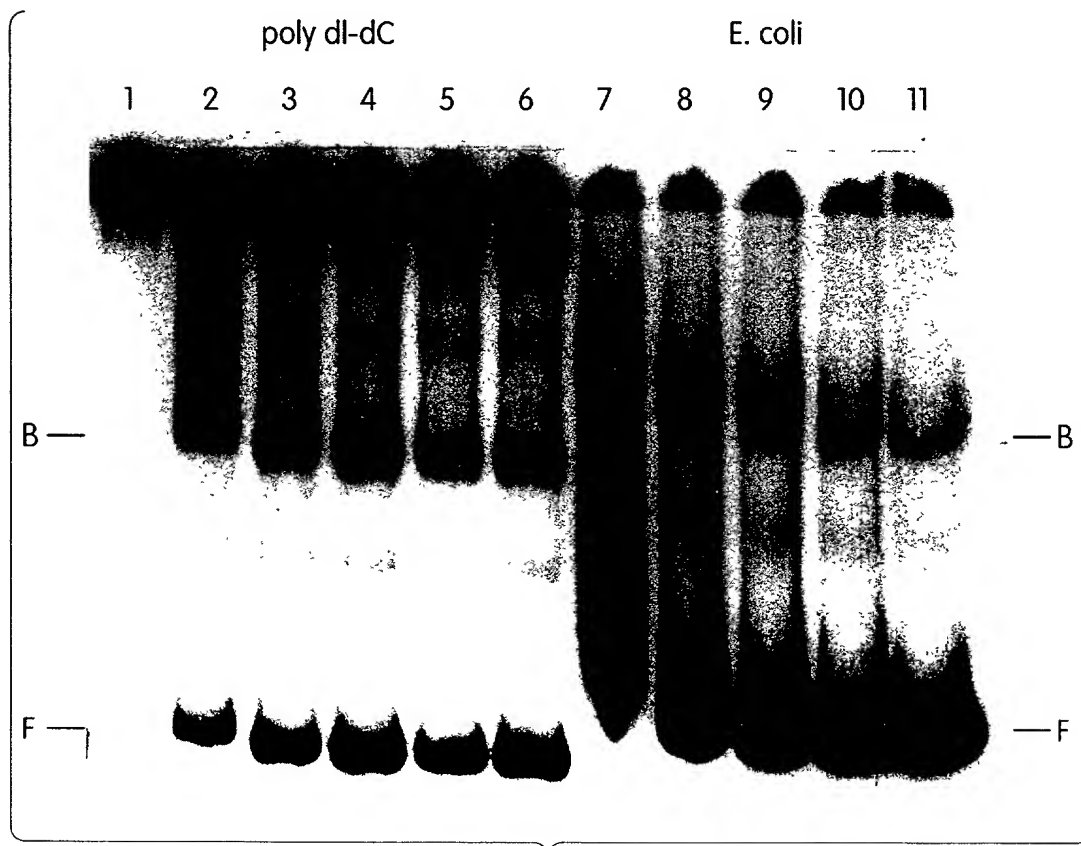


Fig. 1B

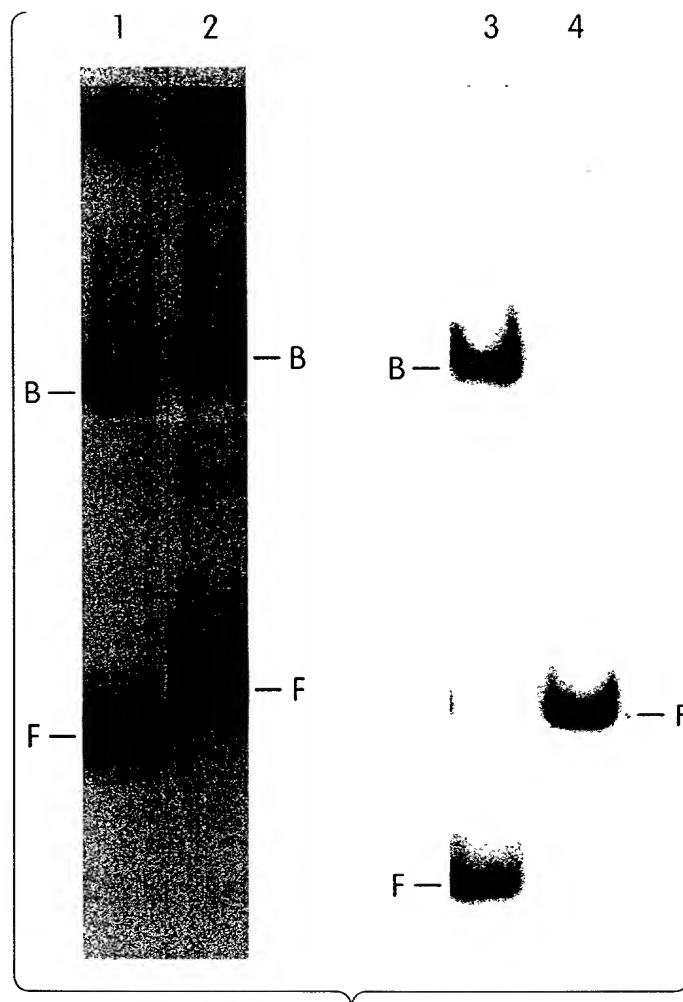


Fig. 1C

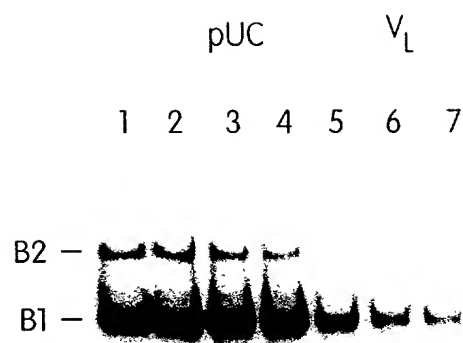
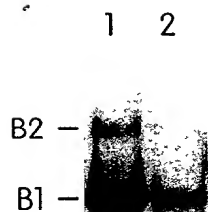


Fig. 2A



HeLa

Fig. 2B



Fig. 3

	*		*
V _L coding strand (-66)	TCTTAATA	ATTTGCAT	ACCCTCAC
V _H non-coding strand (-50)	CGCACATG	ATTTGCAT	ACTCATGA
J _H - C _μ coding strand (166)	CCTGGGTA	ATTTGCAT	TTCTAAAA

Fig. 4A

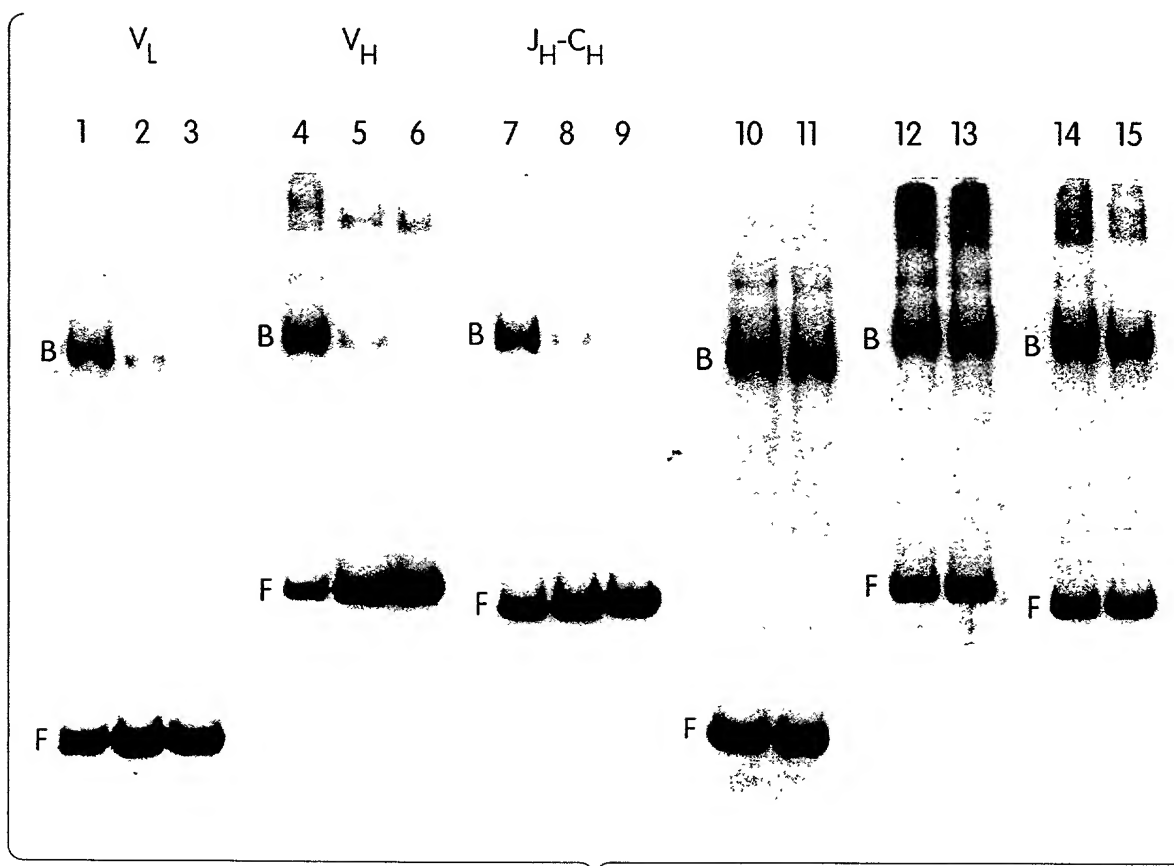


Fig. 4B

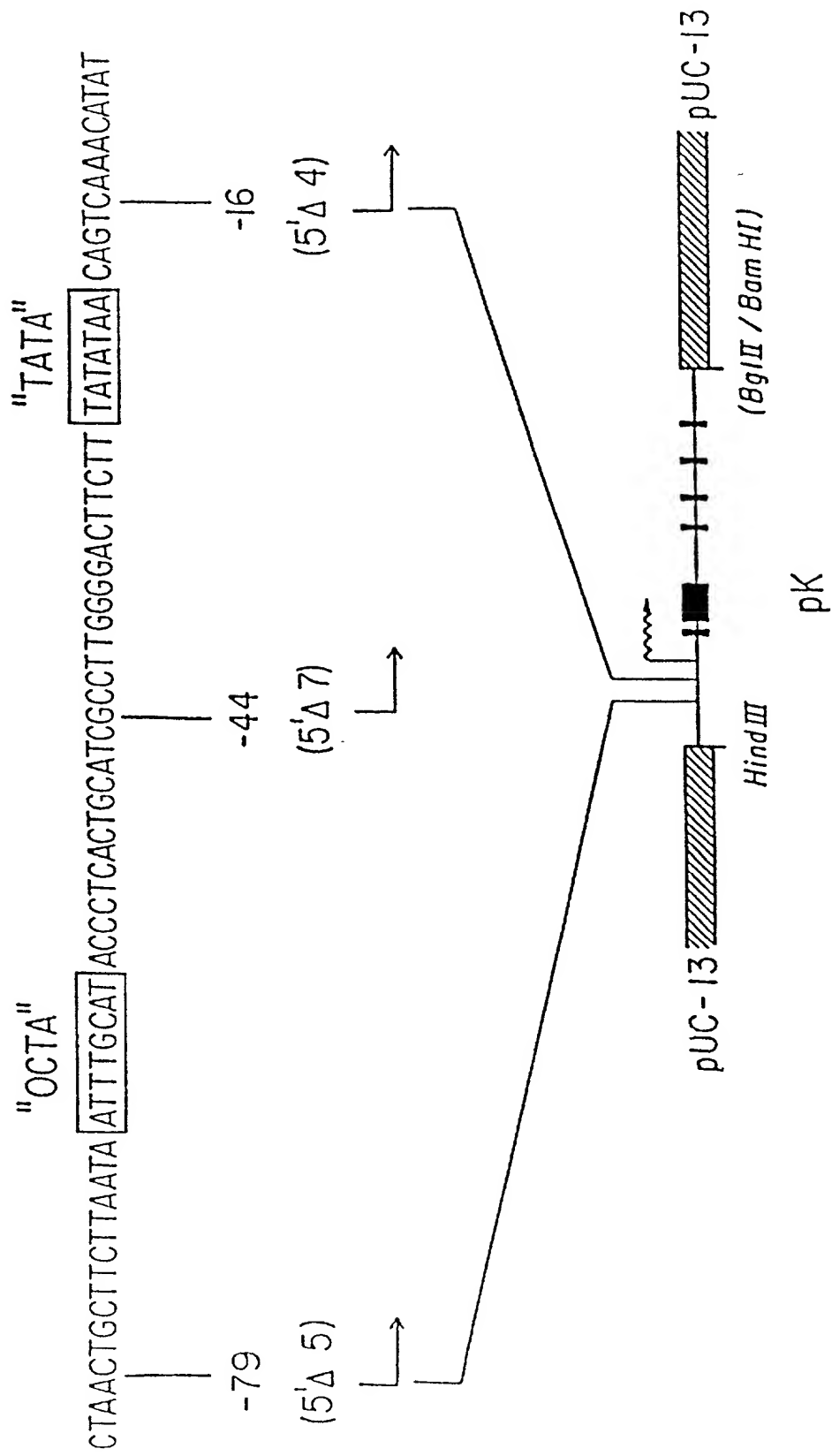


Fig. 5A

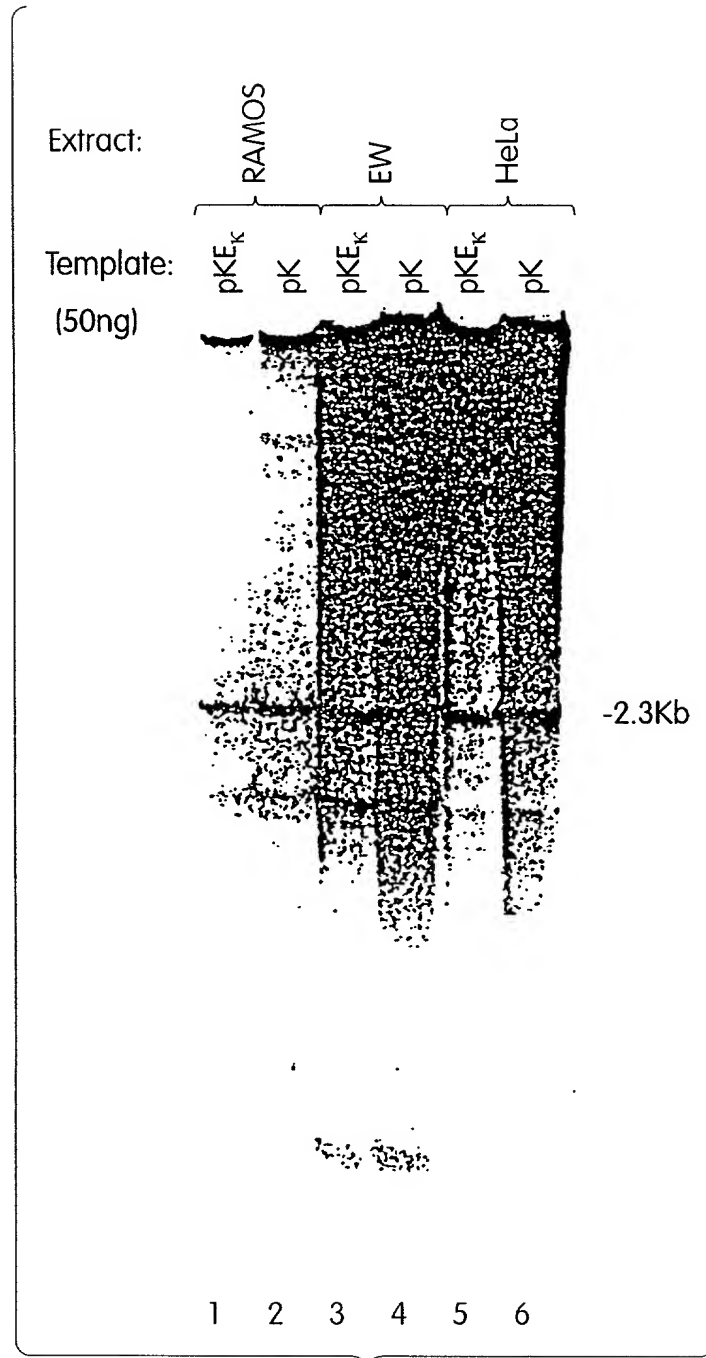


Fig. 5B

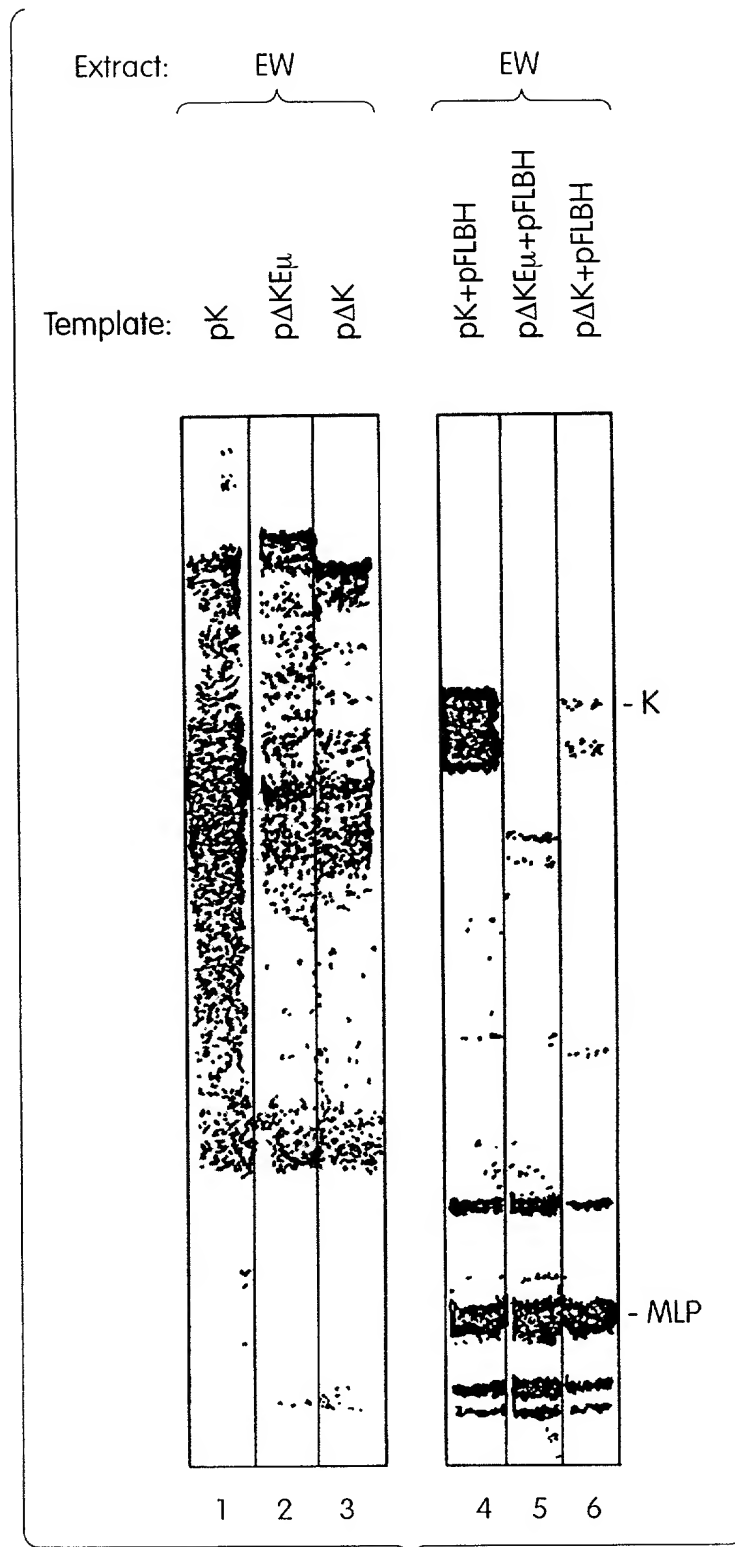


Fig. 6

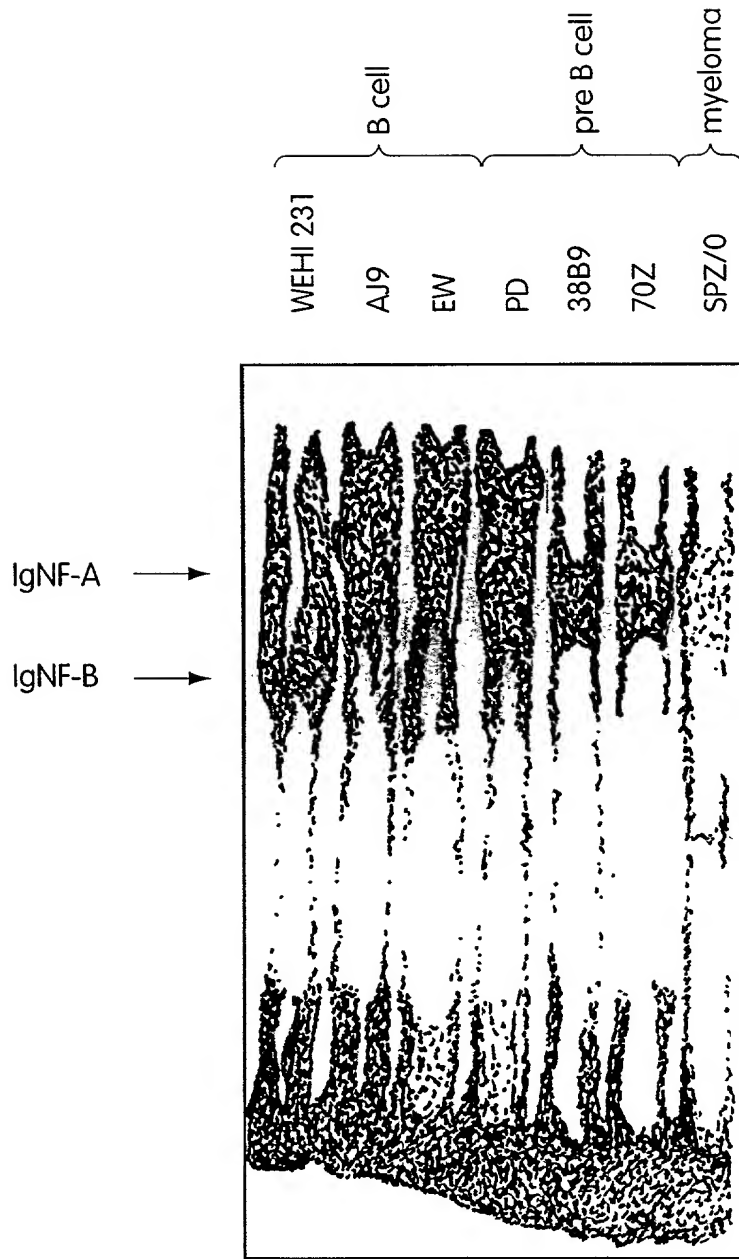


Fig. 7

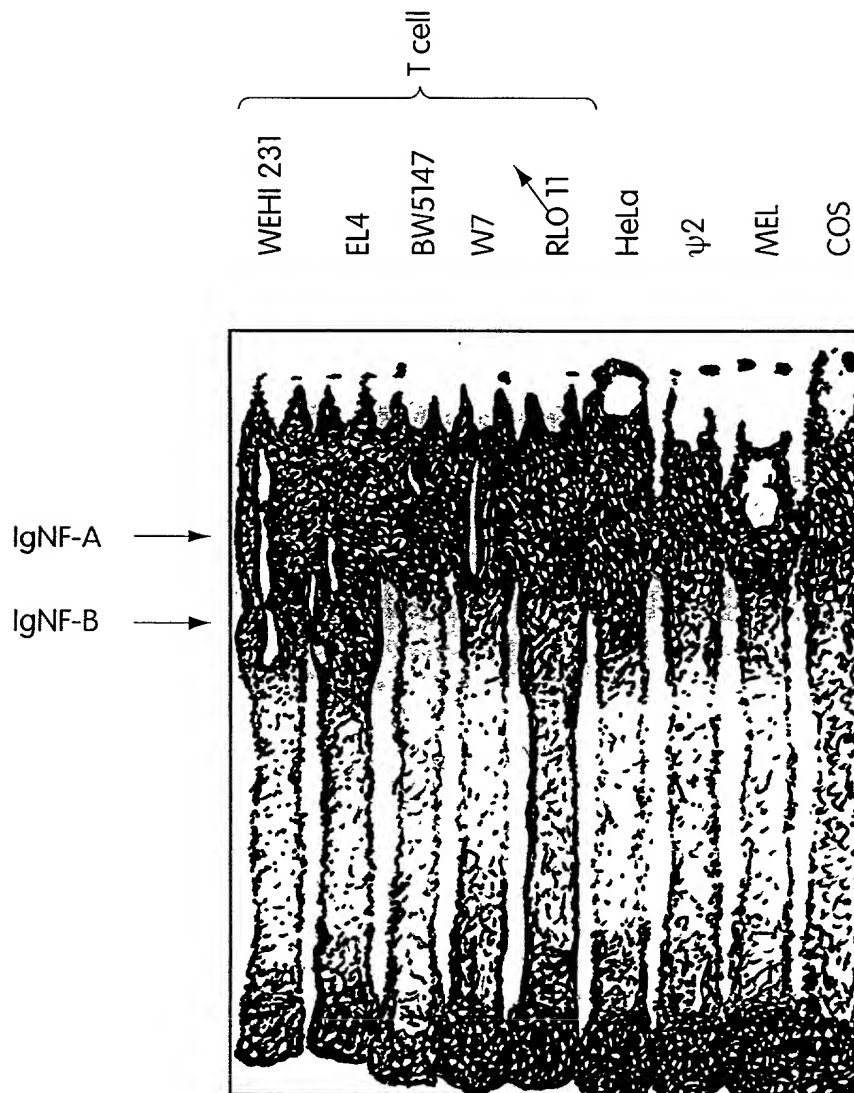


Fig. 8

Figure 9A

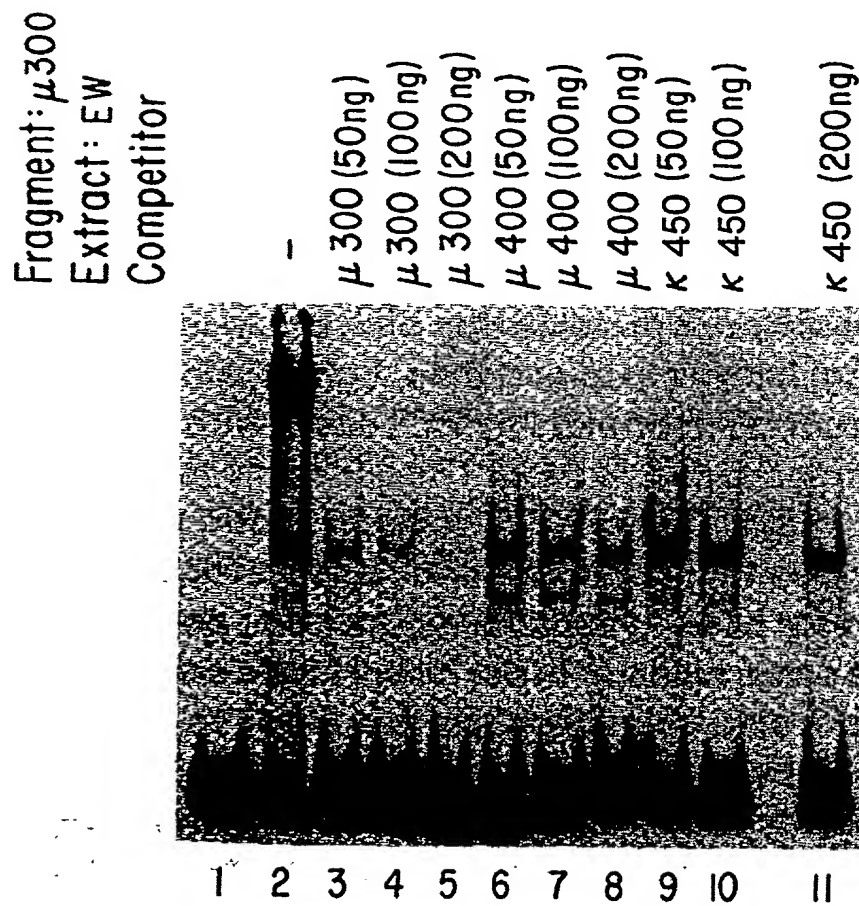
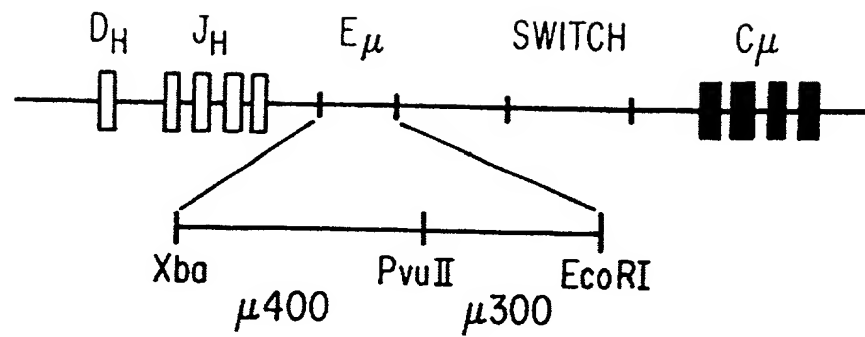


Figure 9B

Figure 10A

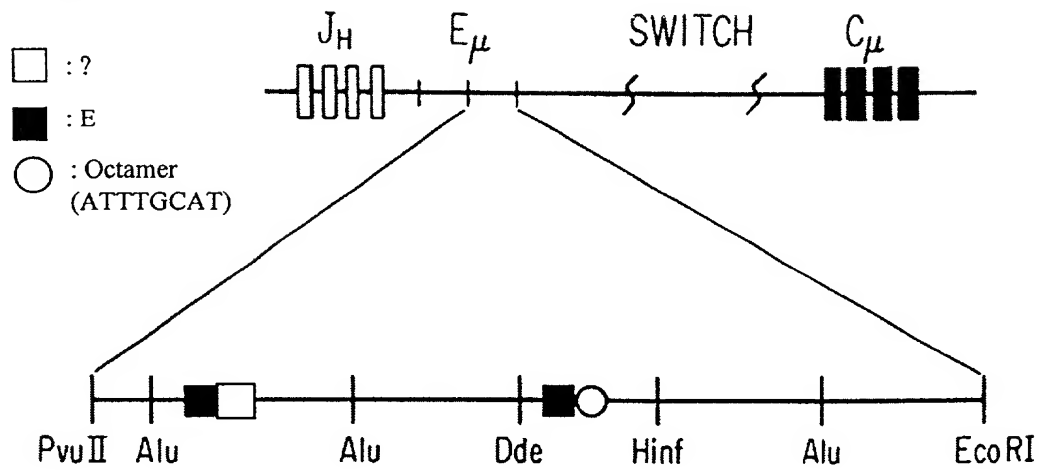
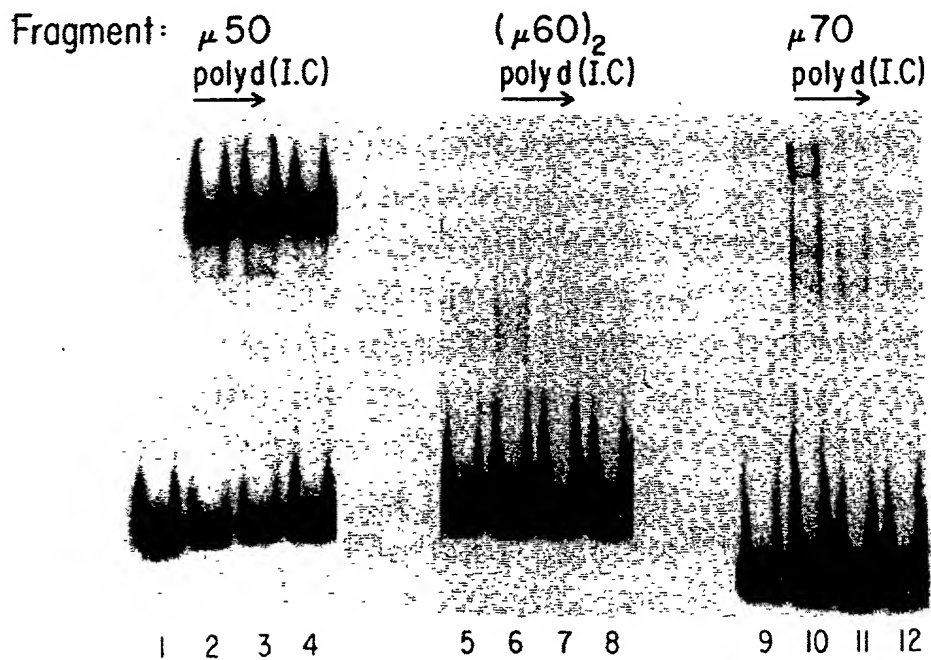


Figure 10B



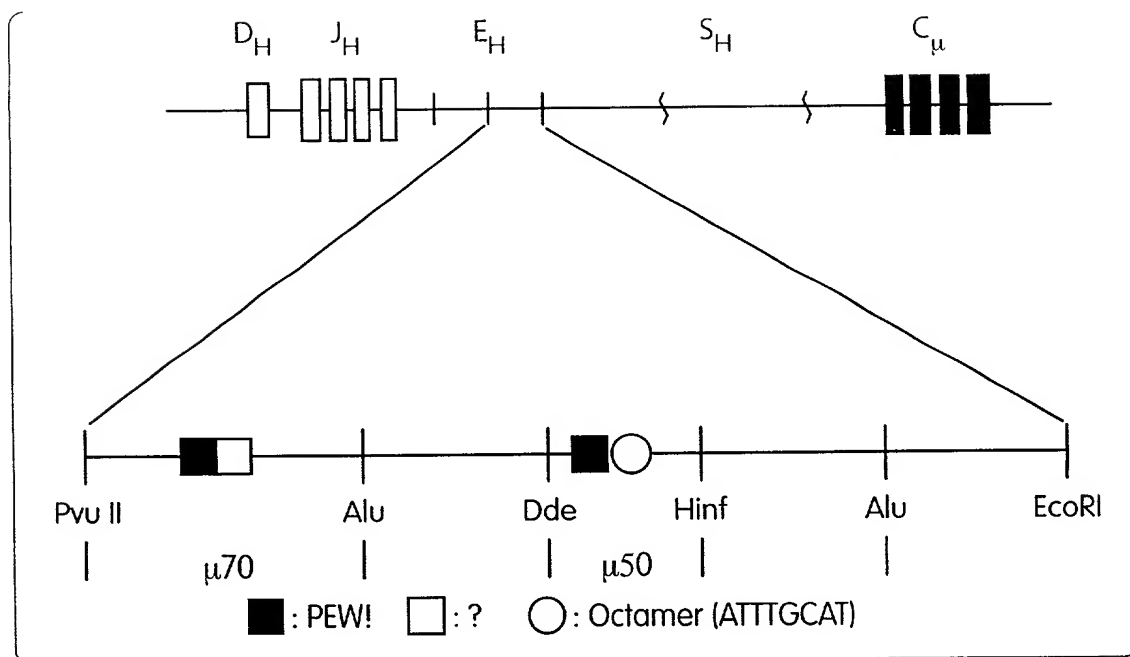


Fig. 10C

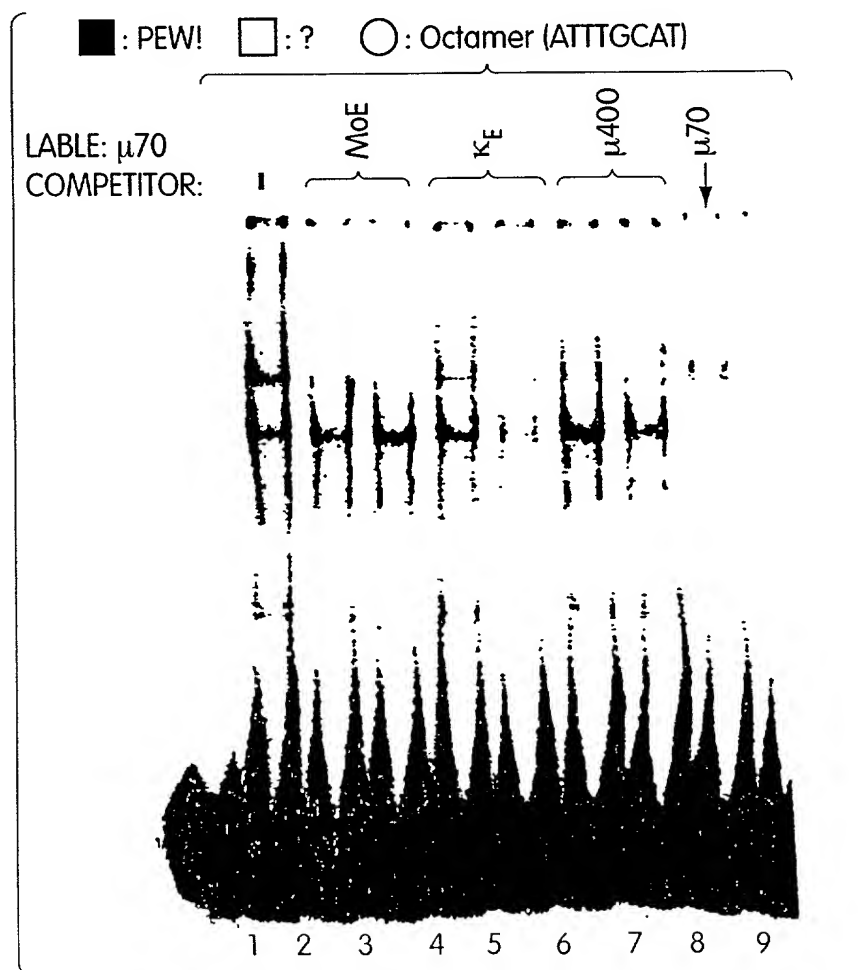


Fig. 10D

Figure 10E

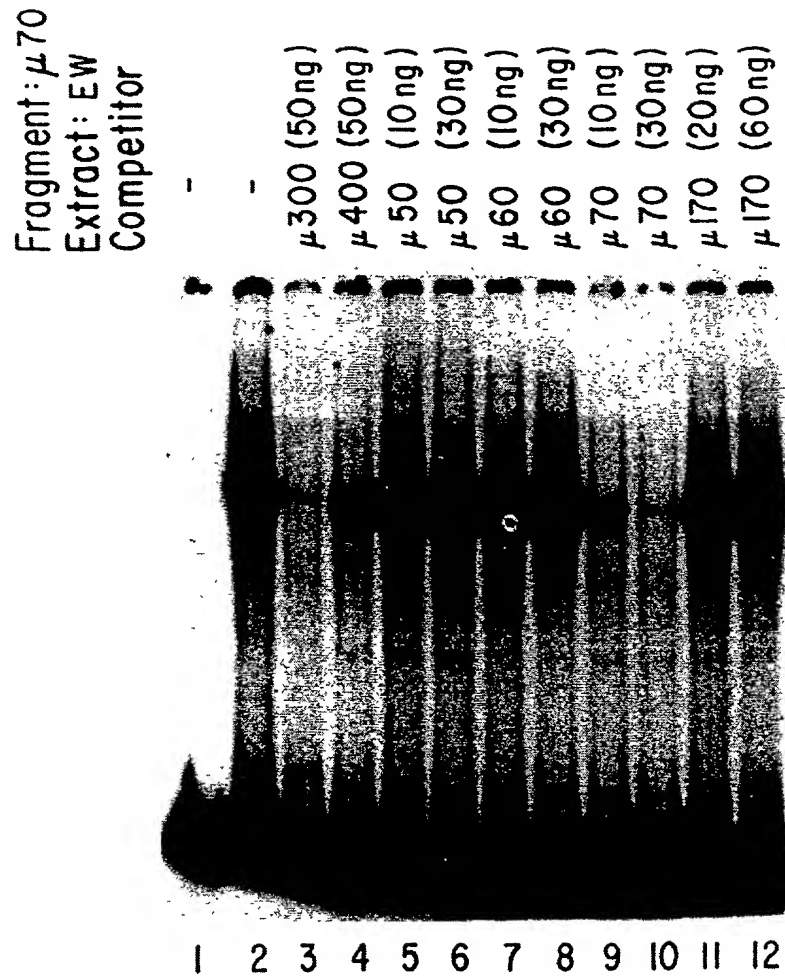


Figure 11A



Figure 11B



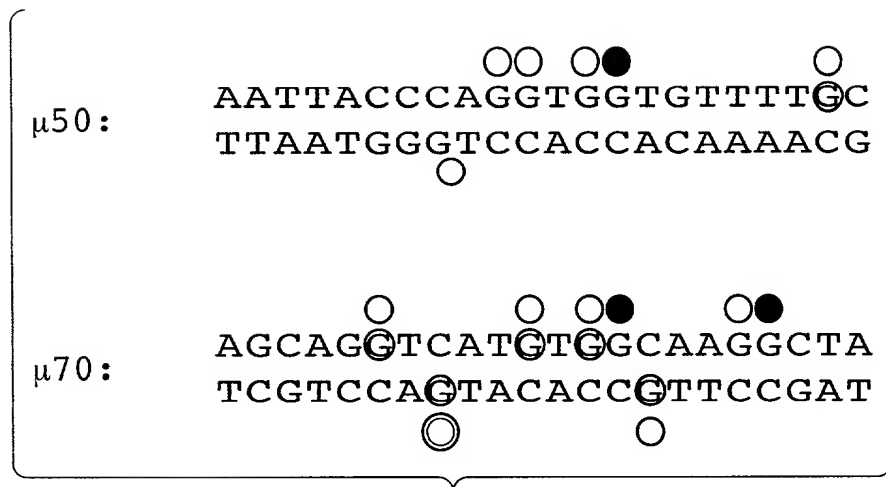


Fig. 11C

Figure 12A

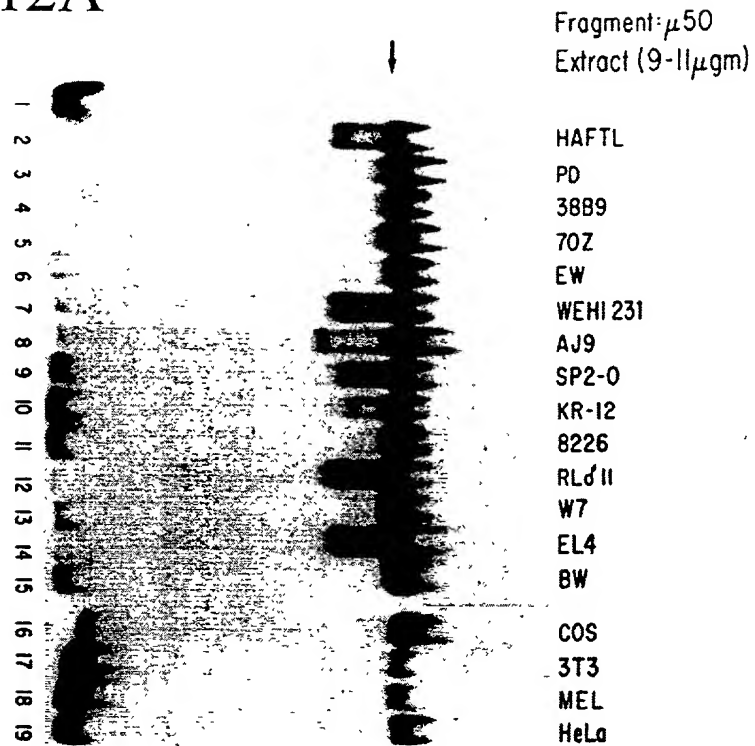


Figure 12B

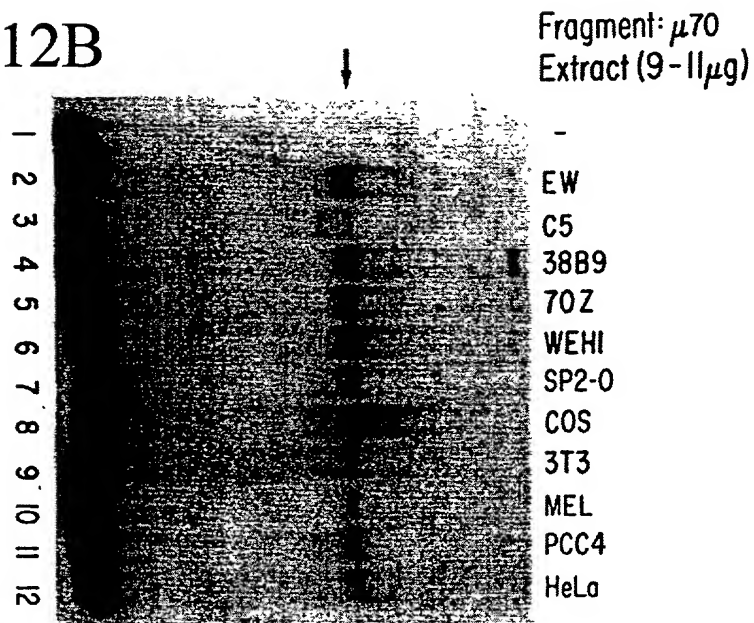


Figure 13A

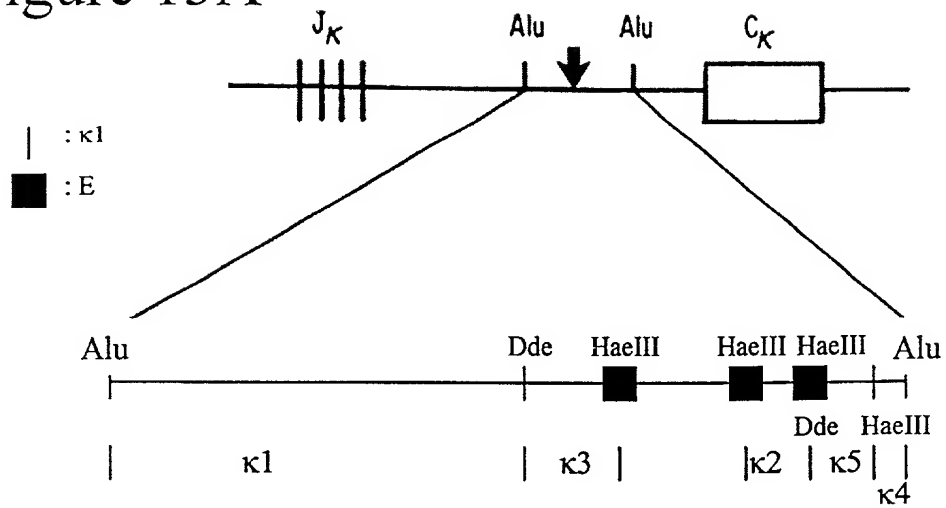


Figure 13B



Figure 13C

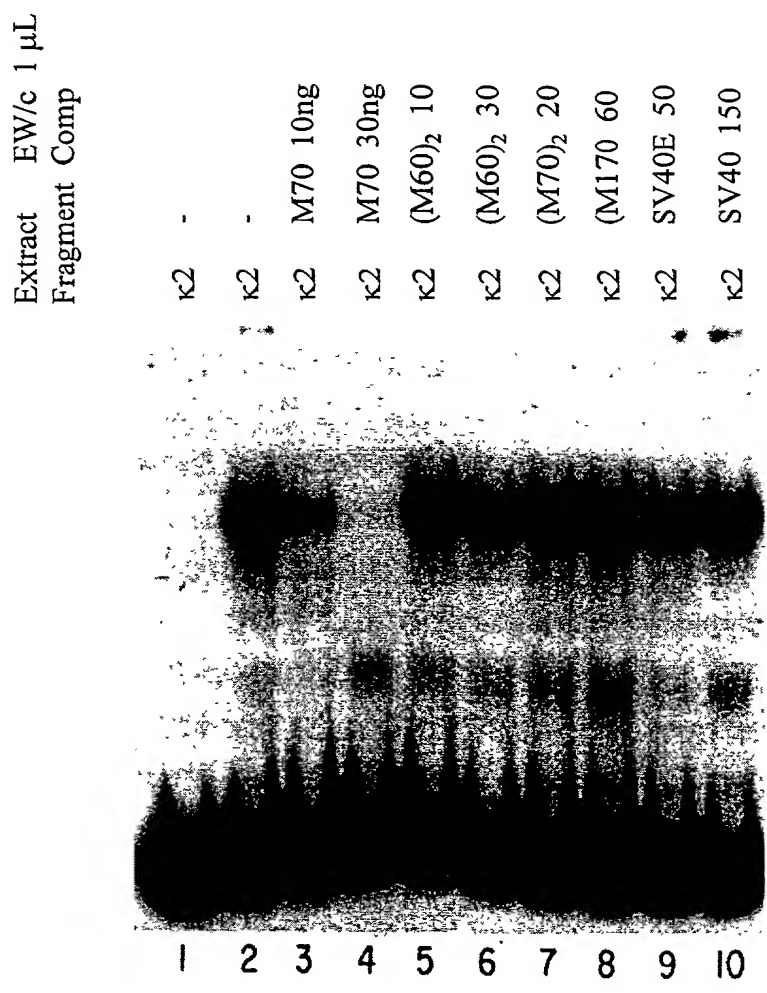
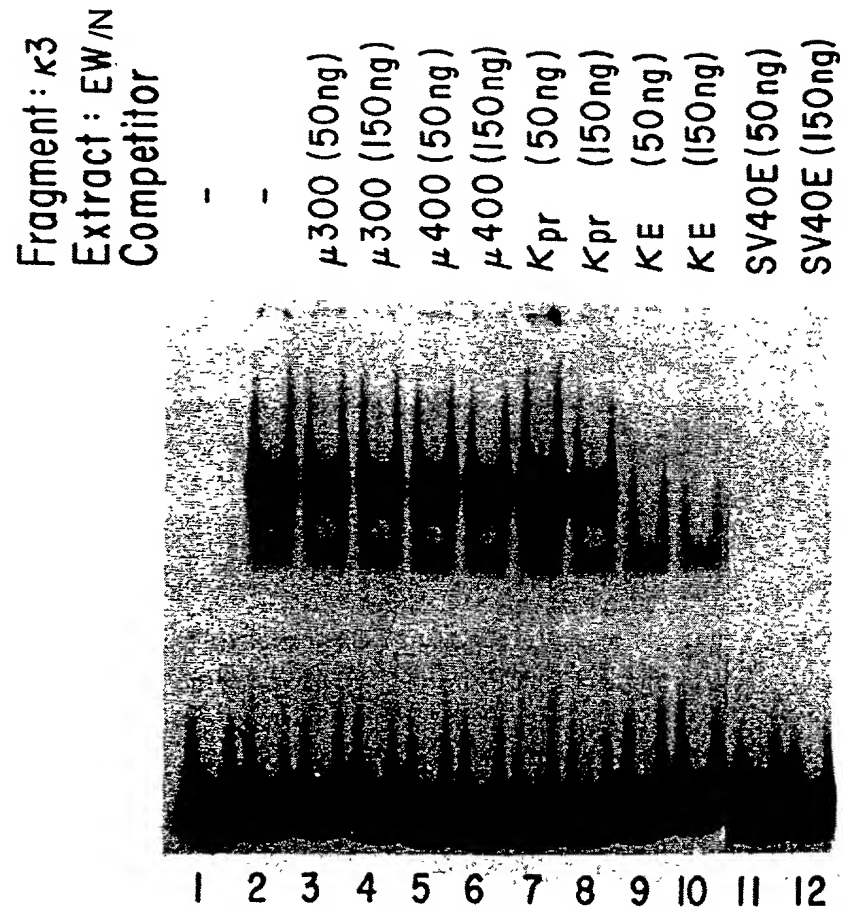


Figure 13D



Fragment: κ -3 /Dde*
Extract

MPCII
-
WEHI 231
-



1 2 3 4

Figure 14

Figure 15A

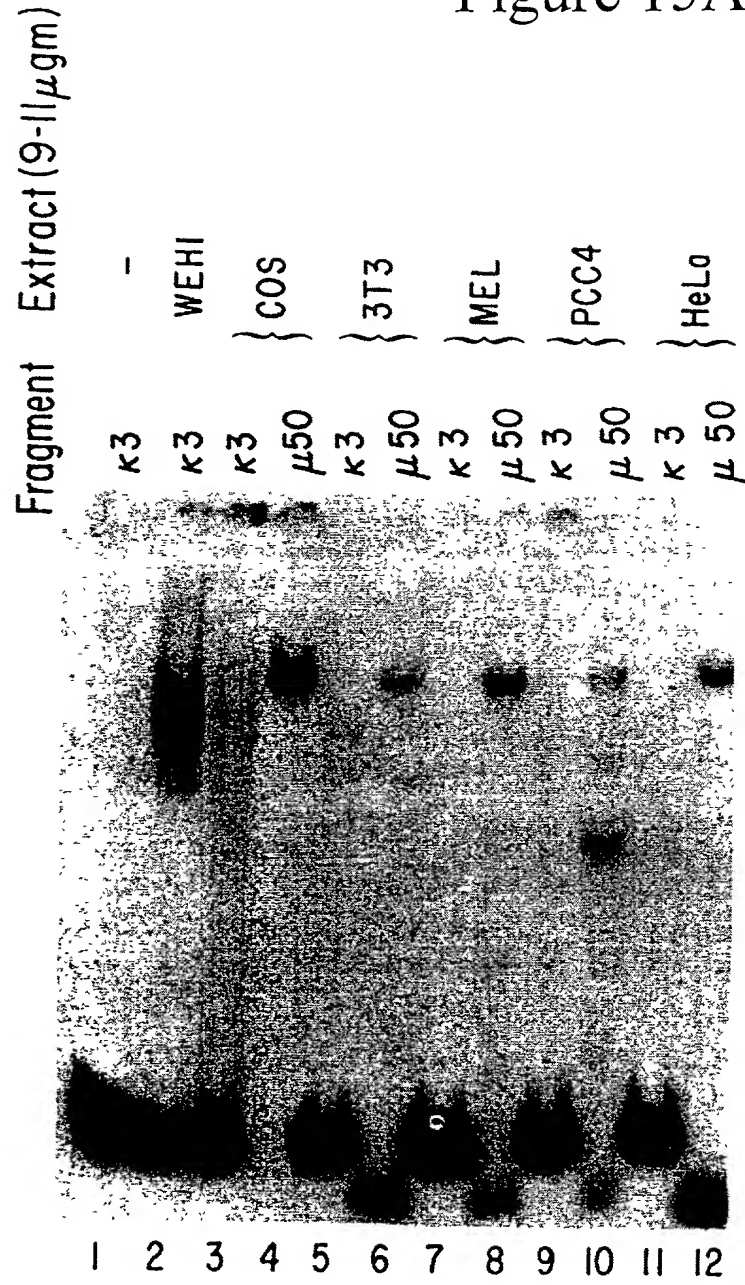
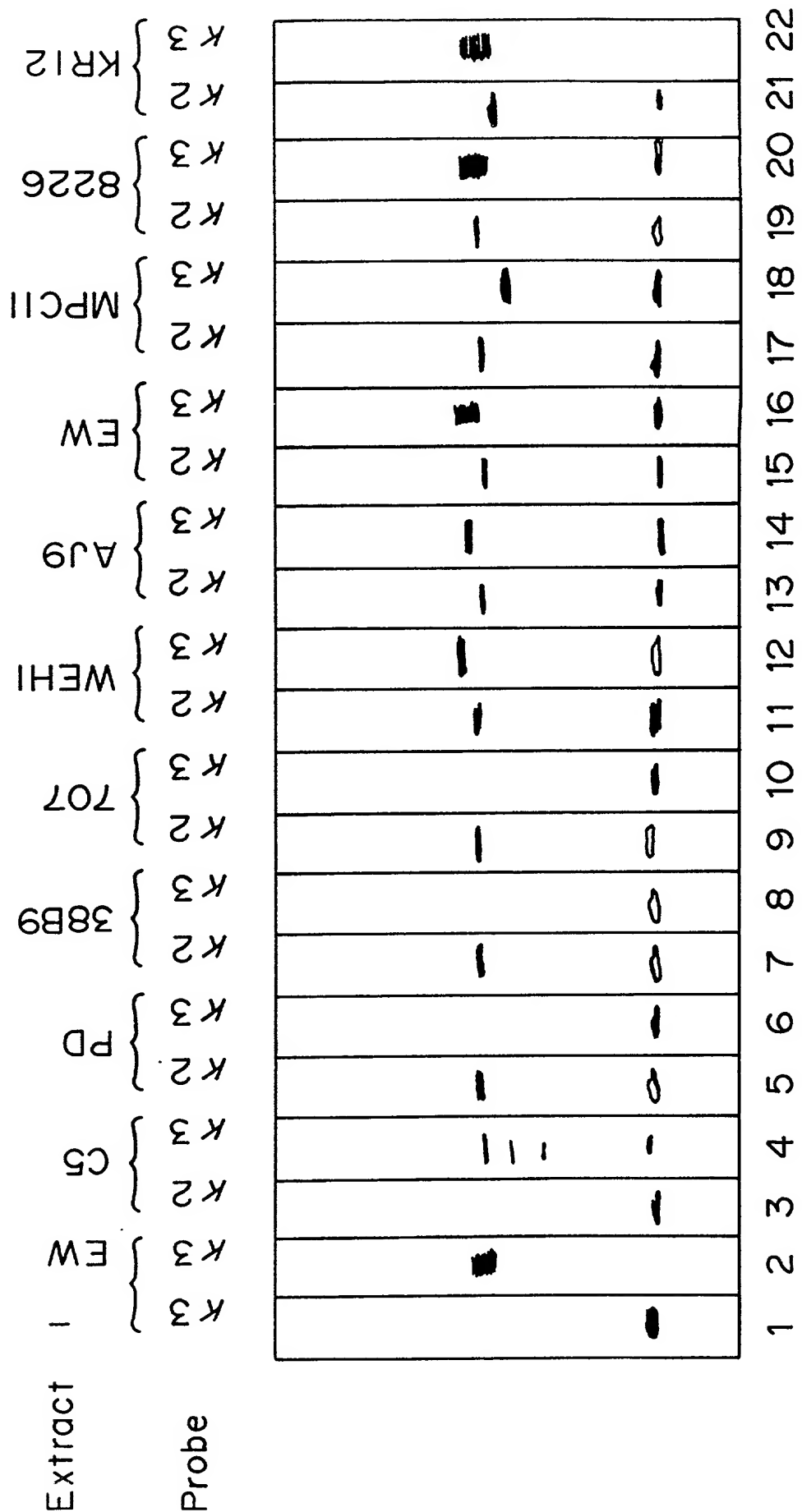


FIGURE 15b



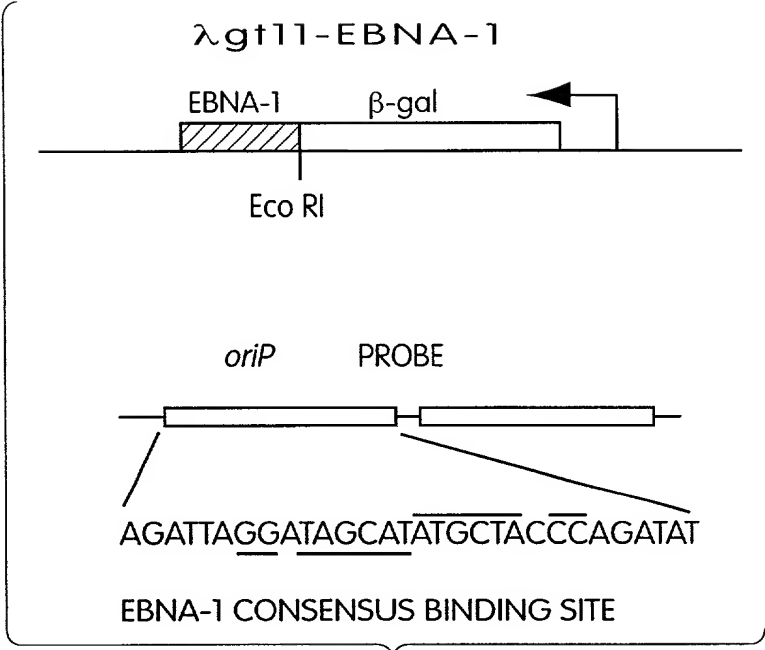


Fig. 16

MHC	<u>TGGGGATTCCCCA</u>
mhc1	TGcGGATTCCCcA
κ EN	aGGGGACTttCCg
κ en	aaattAcTttCCg
	a
SVEN	TGGGGAcTttCCA
HIV	TGGGGAcTttCCA
	aaGGGAcTttCCg

Fig. 17

CTGGGGCCCCCAGAGAGGGTGGGGAGATGACACAGTTGTTCCCCCAGCCCTGGCGGGGGCG
 1 -----+-----+-----+-----+-----+-----+-----+

GGCAGCATGGTTCACTCCAGCATGGGGGCTCCAGAAATAAGAATGTCTAAGCCCCTGGAG
 61 -----+-----+-----+-----+-----+-----+-----+
 M V H S S M G A P E I R M S K P L E

GCCGAGAAGCAAGGTCTGGACTCCCCATCAGAGCACACAGACACCGAAAGAAATGGACCA
 121 -----+-----+-----+-----+-----+-----+-----+
 A E K Q G L D S P S E M T D T E R N G P

GACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTCTCCGTGTCCCCAACTGGC
 181 -----+-----+-----+-----+-----+-----+-----+
 D T N H O N P Q N R T S P F S V S P T G

CCCAGTACAAAGATCAAGGCTGAAGACCCCAGTGGCGATTTCAGCCCCAGCAGCACCCCTG
 241 -----+-----+-----+-----+-----+-----+-----+
 P S T K I K A E D P S G D S A P A A P L

CCCCCTCAGCCGGCCCAGCCTCATCTGCCCCAGGCCCAACTCATGTTGACGGGCAGCCAG
 301 -----+-----+-----+-----+-----+-----+-----+
 P P Q P A Q P N L P Q A Q L M L T G S Q

CTAGCTGGGGACATACAGCAGCTCCTCCAGCTCCAGCAGCTGGTGCTTGTGCCAGGCCAC
 361 -----+-----+-----+-----+-----+-----+-----+
 L A G D I Q Q L L Q L Q Q L V L V P G H

CACCTCCAGCCACCTGCTCAGTTCCTGCTACCGCAGGCCCAGCAGAGCCAGCCAGGCCTG
 421 -----+-----+-----+-----+-----+-----+-----+
 H L Q P P A Q F L L P Q A Q Q S Q P G L

CTACCGACACCAAATCTATTCCAGCTACCTCAGCAAACCCAGGGAGCTCTTCTGACCTCC
 481 -----+-----+-----+-----+-----+-----+-----+
 L P T P H L F Q L P Q Q T Q G A L L T S

CAGCCCCGGGCGGGCTTCCCACACAGGCCGTGACCCGCCCTACGCTGCCCGACCCGCAC
 541 -----+-----+-----+-----+-----+-----+-----+
 Q P R A G L P T Q A V T R P T L P D P H

CTCTCGCACCCGCAGCCCCCAAATGCTTGGAGCCACCATCCCACCCCGAGGAGCCCAGT
 601 -----+-----+-----+-----+-----+-----+-----+
 L S H P Q P P K C L E P P S H P E E P S

GATCTGGAGGAGCTGGAGCAATTGGCCCGCACCTTCAAGCAACGCCGCATCAAGCTGGGC
 661 -----+-----+-----+-----+-----+-----+-----+
 D L E E L E Q F A R T F K Q R R I K L G

TTCACGCAGGGTGATGTGGGCCTGGCCATGGGCAAGCTCTACGCCAACGACTTCAGCCAG
 721 -----+-----+-----+-----+-----+-----+-----+
 F T Q G D V G L A M G K L Y G N D F S Q
 C G P G H G Q A L R Q R L Q P D

Fig. 18A

781 ACGACCATTTCCTCGAGGCCCTCAACCTGAGCTTCAAGAACATGTGCAAACTCAAG
 -----+-----+-----+-----+-----+-----+
 T T I S R F E A L N L S F K N M C K L K
 D H F P L R G P Q P E L Q E H V Q T Q A

 841 CCCCTCCTGGAGAAGTGGCTCAACGATGCAGAGACTATGTCTGTGGACTCAAGCCTGCCC
 -----+-----+-----+-----+-----+-----+
 P L L E K W L N D A E T M S V D S S L P
 P P G E V A Q R C R D Y V C G L K P A Q

 901 AGCCCCAACCAGCTGAGCAGCCCCAGCCTGGGTTTCGAGCCTGCCGGCCGGAGACGCAAG
 -----+-----+-----+-----+-----+-----+
 S P N O L S S P S L G F E P A G R R R K
 P Q P A E Q P Q P G F R A C M P E T Q E

 961 AAGAGGACCAGCATCGAGACAAACGTCCTCGCCTTAGAGAAGAGTTTTCTAGCGAAC
 -----+-----+-----+-----+-----+-----+
 K R T S I E T N V R F A L E K S F L A N
 E D Q M R D K R P L R L R E E F S S E P

 1021 CAGAAGCCTACCTCAGAGGAGATCCTGCTGATCGCCGAGCAGCTGCACATGGAGAAGGAA
 -----+-----+-----+-----+-----+-----+
 Q K P T S E E I L L I A E Q L H M E K E
 E A Y L R G D P A D R R A A A H G E G S

 1081 GTGATCCGCGTCTGGTTCTGCAACCGGCCCCAGAAGGACAAACGCATCAACCCCTGCAGT
 -----+-----+-----+-----+-----+-----+
 V I R V W F C N R R Q K E K R I H P C S
 D P R L V L Q P A P E G E T H Q P L Q C

 1141 GCGGCCCCCATGCTGCCCAGCCCAGGGAAGCCGGCCAGCTACAGCCCCCATATGGTCACA
 -----+-----+-----+-----+-----+-----+
 A A P M L P S P G K P A S Y S P H H V T
 G P H A A Q P R E A G Q L Q P P Y G H T

 1201 CCCCAAGGCGGCGGGGACCTTACCGTTGTCCCAAGCTTCCAGCAGTCTGAGCACAACA
 -----+-----+-----+-----+-----+-----+
 P Q G G A G T L P [L] S Q A S S S [L] S T T
 P A G R G D L T V V P S F Q Q S E H N S

Fig. 18A
(CONTINUED)

GTTACTACCTTATCCTCAGCTGTGGGGACGCTCCACCCCAGCCGGACAGCTGGAGGGGGT
 1261 -----+-----+-----+-----+-----+-----+-----+
 V T T [L] S S A V G T [L] H P S R T A G G G
 Y Y L I L S C G D A P P Q P D S N M G W
 GGGGGCGGGGGCGGGGCTGCGCCCCCTCAATTCCATCCCCTCTGTCACTCCCCACCC
 1321 -----+-----+-----+-----+-----+-----+-----+
 G G G G G A A P P L N S I P S V T P P P
 G M G R G C A P P Q F H P L C H S P T P
 CCGGCCACCACCAACAGCACAAACCCAGCCCTCAAGGCAGCCACTCGGCTATCGGCTTG
 1381 -----+-----+-----+-----+-----+-----+-----+
 P A T T N S T N P S P Q G S H S A I G L
 G H N Q Q H K P Q P S R Q P L G Y M L V
 TCAGGCCTGAACCCCAGCACGGGGTAAGTGGGTGCACGTGGGAAGCTGTGGGGAGAAGCA
 1441 -----+-----+-----+-----+-----+-----+-----+
 S G L H P S T G +
 A P E P Q N G V S G C T W E A V G R S R
 GCGTCGCTGCTCCTTCTAGGGTGGGGAGCGGCACCCCAGTTATGTTGGCAGGTCCCTGCC
 1501 -----+-----+-----+-----+-----+-----+-----+
 V A A A S R V G S G T P V M L A G P C P
 CCTGCTAATGCCTCTGCTTTGCCTCTTGCAGAAGCACAAATGGTGGGGTTGAGCTCCGGCT
 1561 -----+-----+-----+-----+-----+-----+-----+
 C +
 GAGTCCAGCCCTCATGAGCAACAACCCTTTGGCCACTATCCAAGGTGCGTGCTGCCTCAT
 1621 -----+-----+-----+-----+-----+-----+-----+
 GTCACACCCATCGTCACCAGCCCCGGAATTCGAG
 1681 -----+-----+-----+-----+-----+-----+-----+

Fig. 18A
(CONTINUED)

CCTCAAGGCAGCCACTCGGGCTATCGGCTTGTTCAGGCCTGAACCCCAGCACGGGGCCCTGGC
 1411 -----+-----+-----+-----+-----+-----+-----+
 P Q G S H S A I G L S G L N P S T G P G
 S A Q P L G Y R L V M P E P Q M G P N P

CTCTGGTGGAACCCTGCCCCCTTACCAGCCTTGATGGCAGCGGGAATCTGGTGCTGGGGGC
 1471 -----+-----+-----+-----+-----+-----+-----+
 L W W N P A P Y Q P .
 L V E P C P L P A L M A A G I W C W G Q

AGCCGGTGCAGCCCCGGGGAGCCCTGGCCTGGTGACCTCGCCGCTCTTCTTGAATCATGC
 1531 -----+-----+-----+-----+-----+-----+-----+
 P V Q P R G A L A W .

TGGGCTGCCCCCTGCTCAGCACCCCGCCTGGTGTGGGCCTGGTCTCAGCAGCGGCTGCGGG
 1591 -----+-----+-----+-----+-----+-----+-----+
 TGTGGCAGCCTCCATCTCCAGCAAGTCTCCTGGCCTCTCCTCCTCATCCTCTTCATCCTC

ATCCTCCTCCTCCTCCACTTGCAGCGAGACGGCAGCACAGACCCTGGAGGTCCAGGGGGG
 1711 -----+-----+-----+-----+-----+-----+-----+
 CCCGAGGCAGGGTCCAAACCTGAGTGAGGGCCAGCCATGCCTCCCCTCCCATTCTCTGG

TCCCTGCCCCGGAATTC
 1831 -----+-----

Fig. 18B

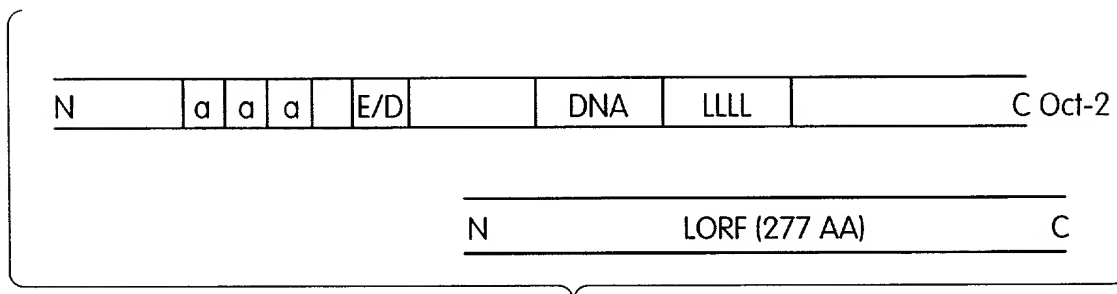


Fig. 18C

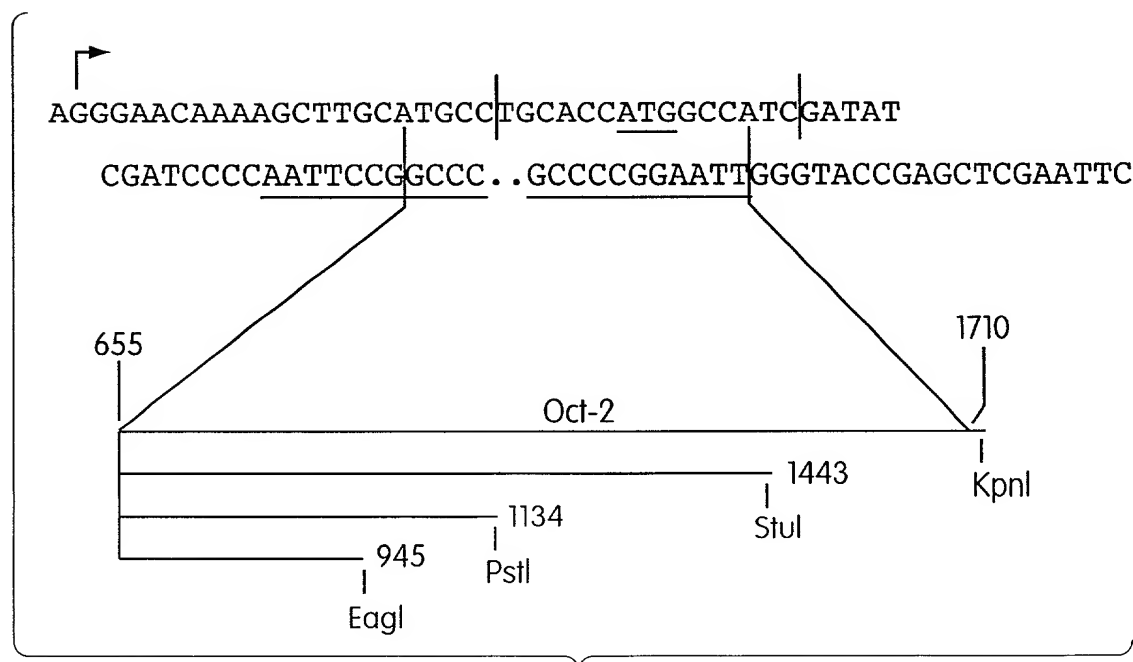


Fig. 19

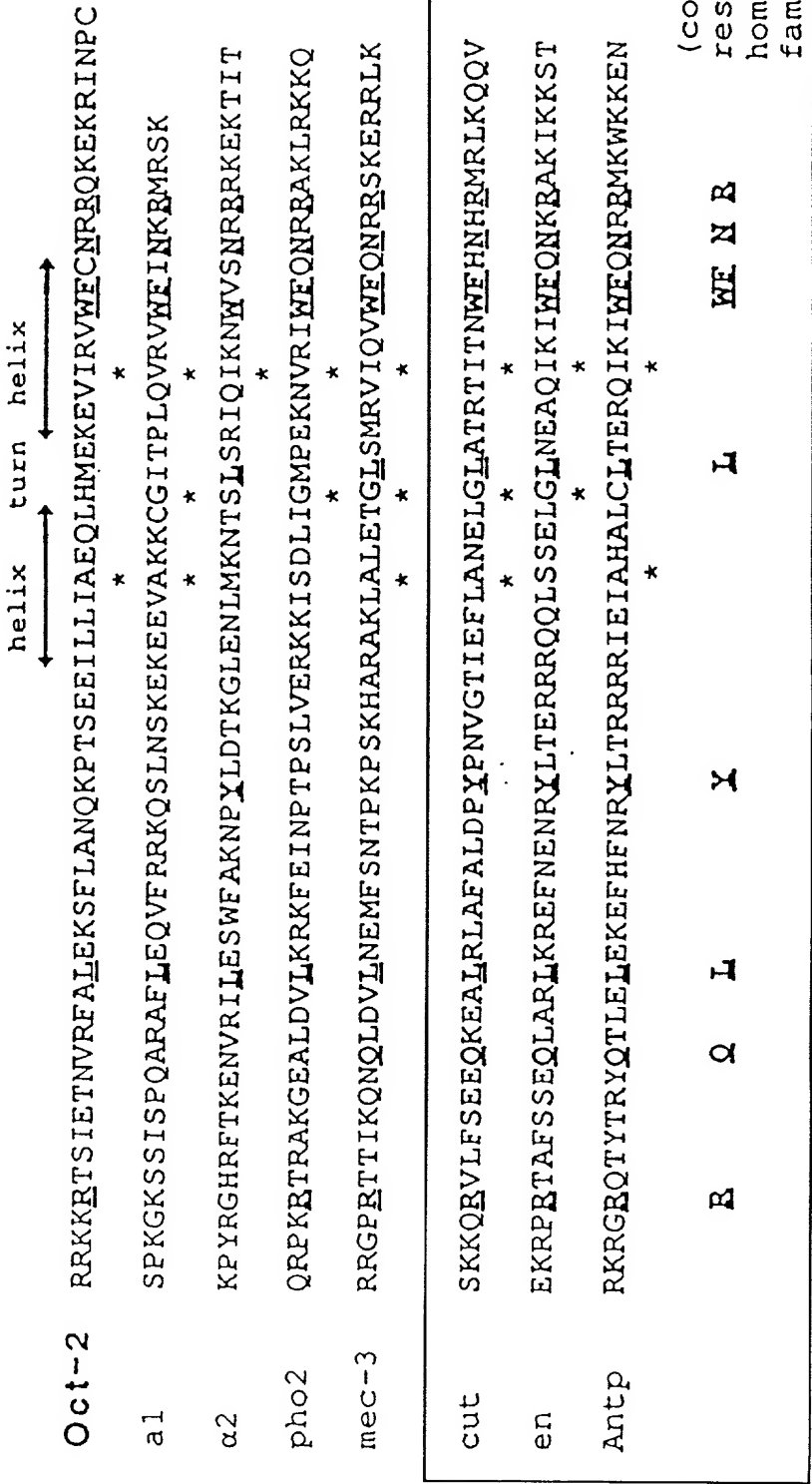


Fig. 20

Figure 21A

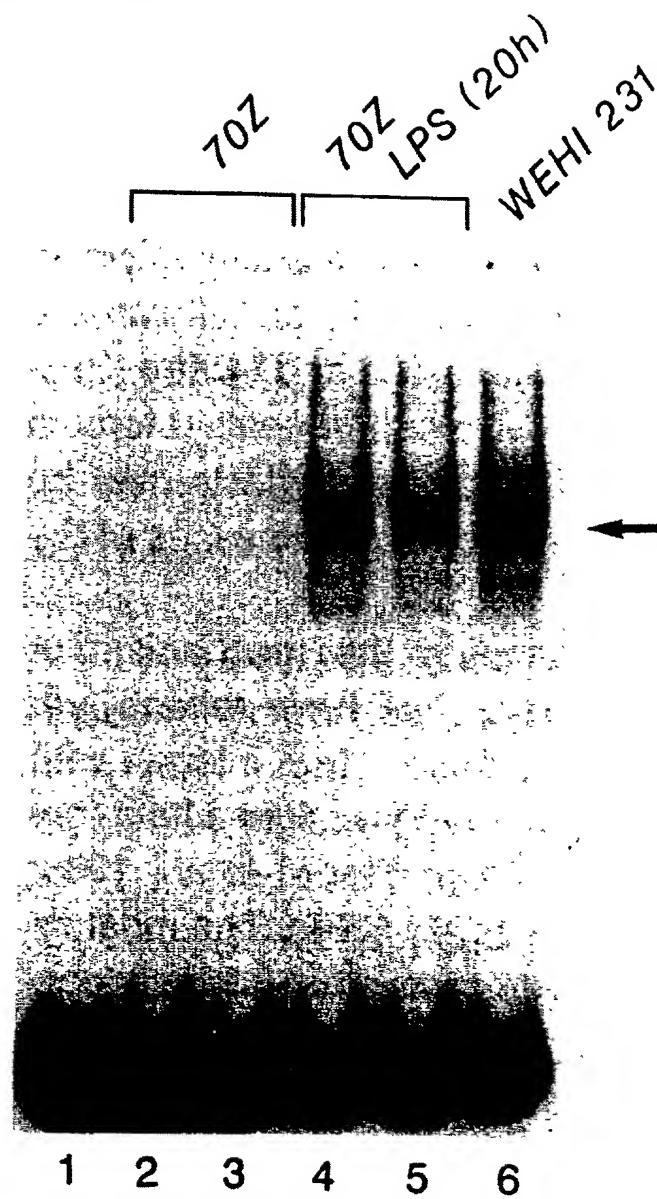


Figure 21B

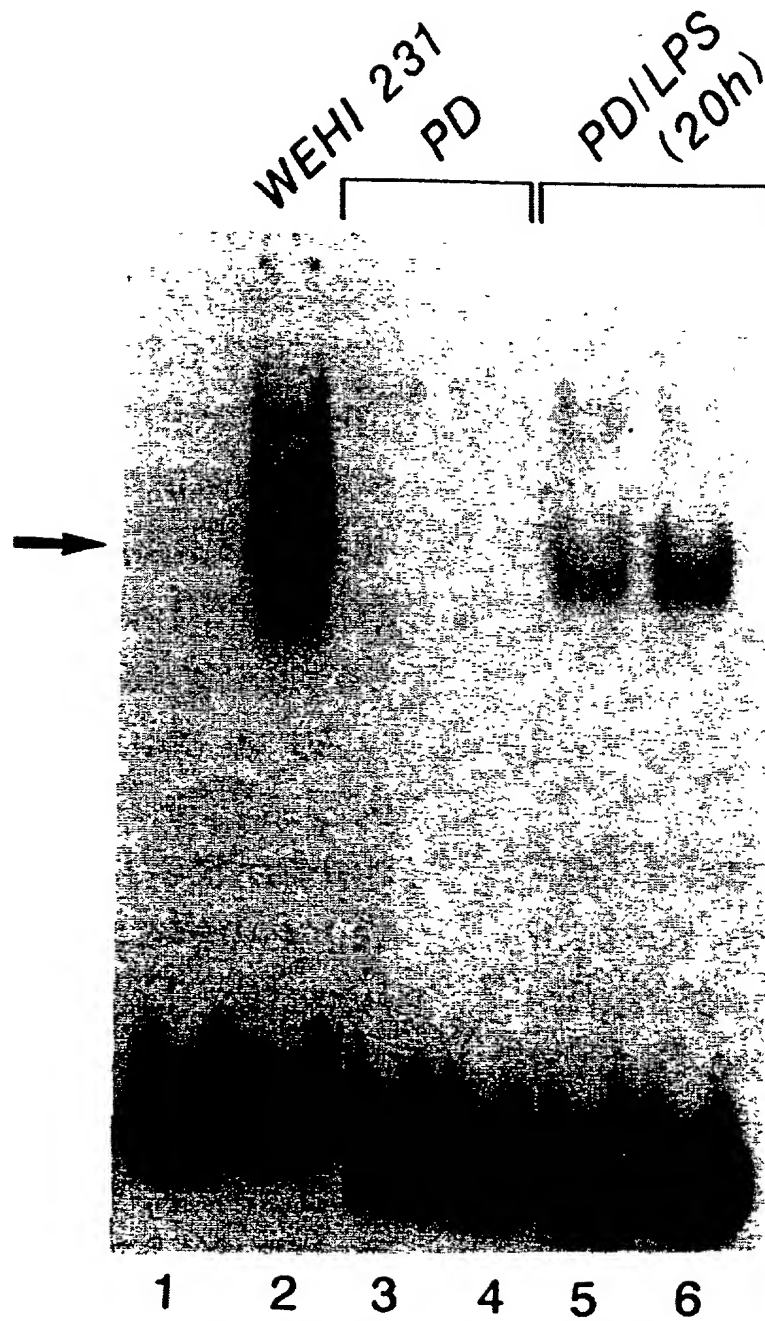


Figure 22A

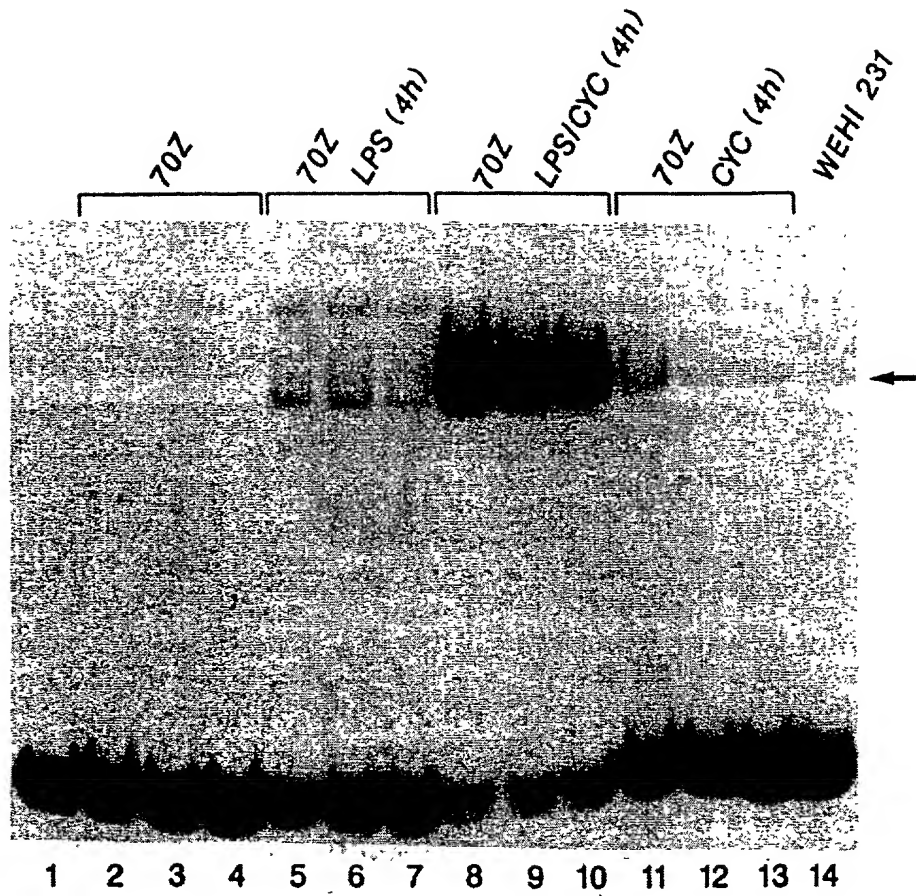


Figure 22B

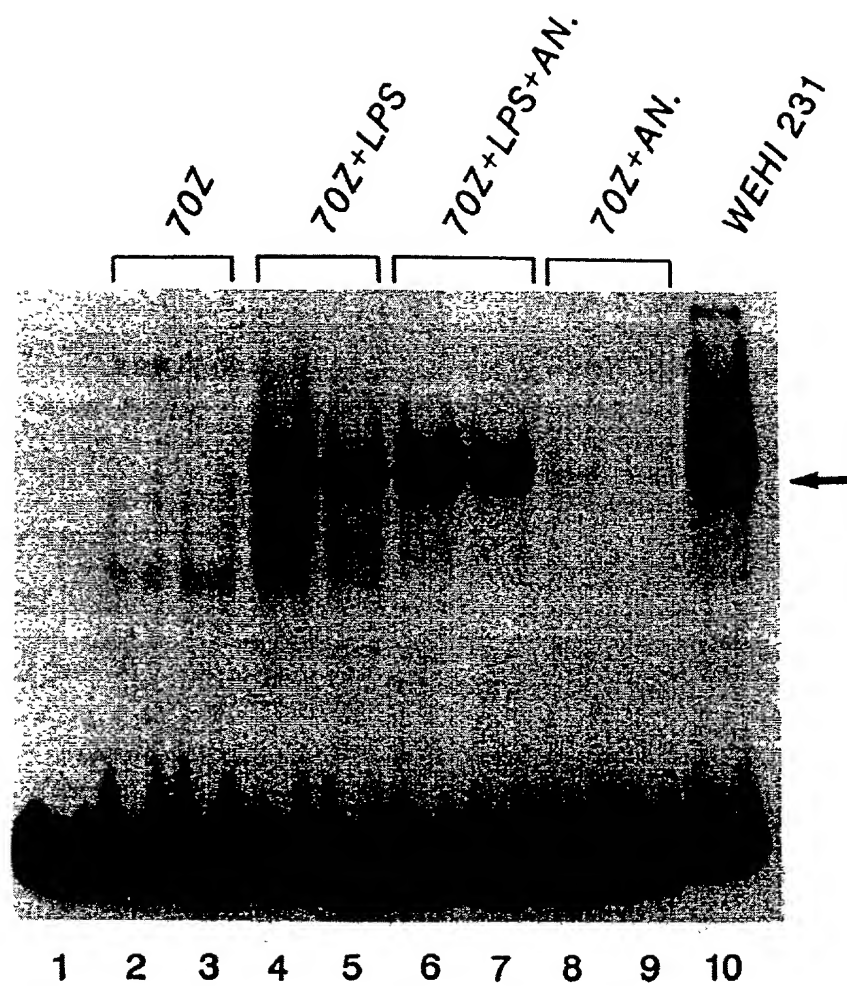


Figure 23A

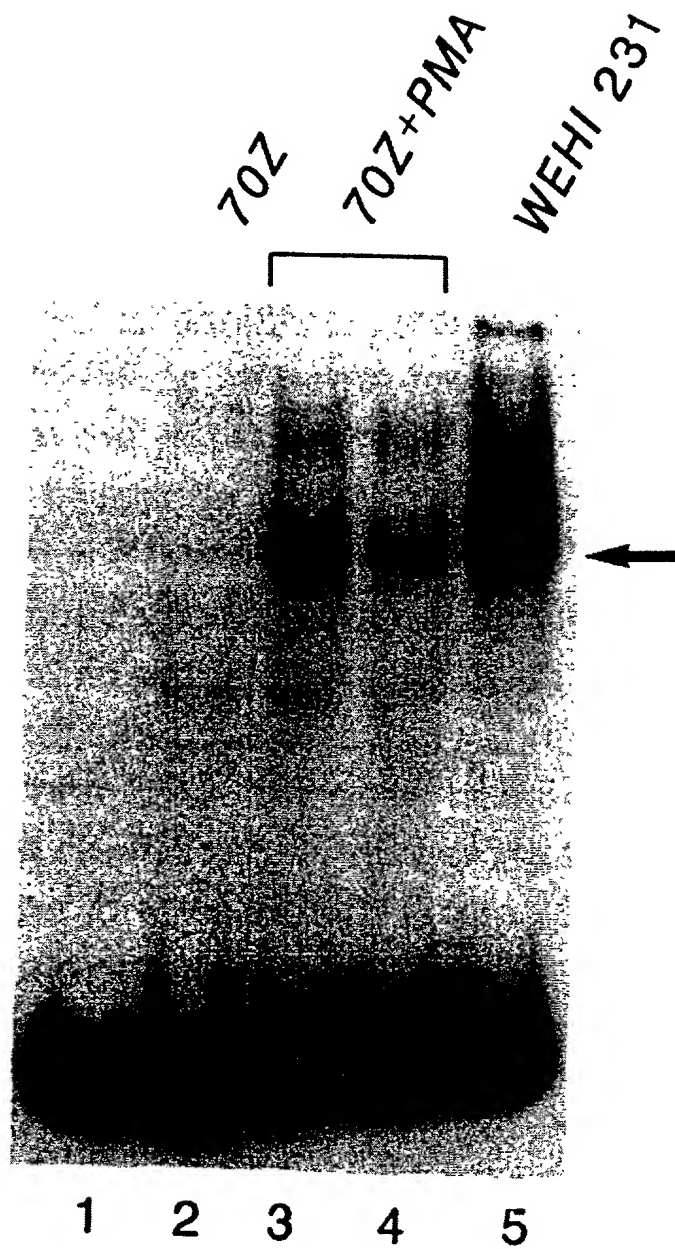


Figure 23B

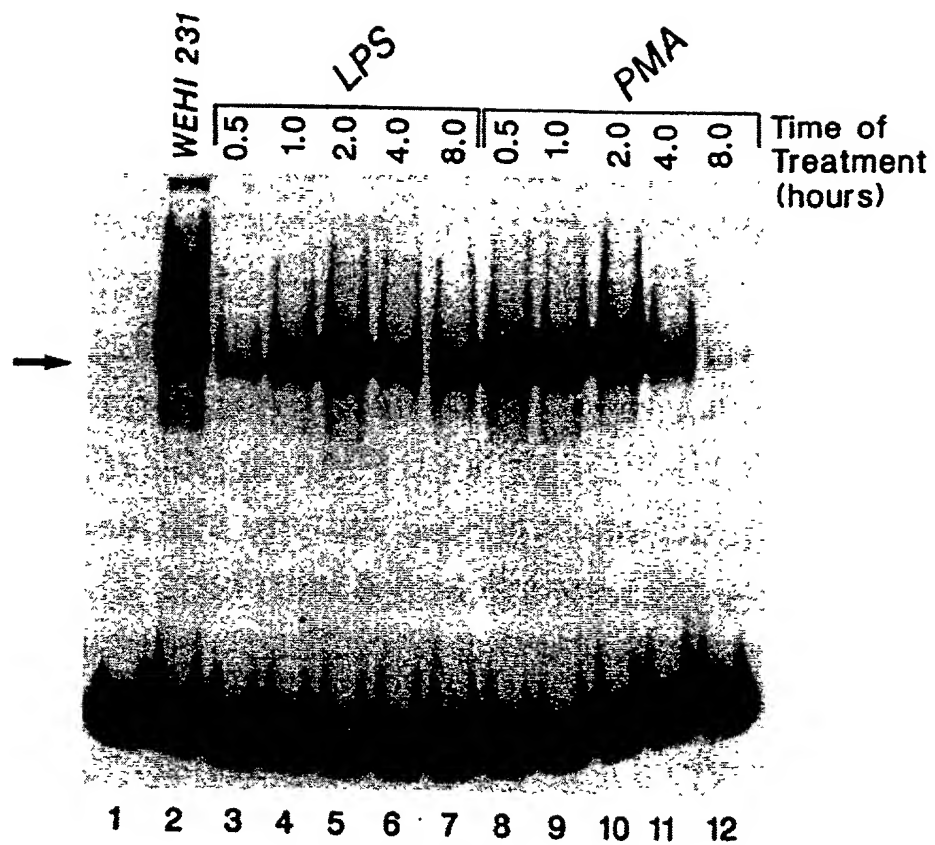


Figure 24A

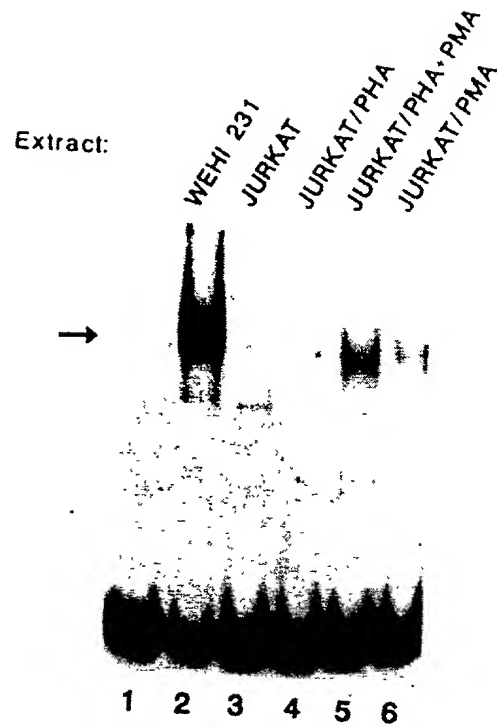


Figure 24B

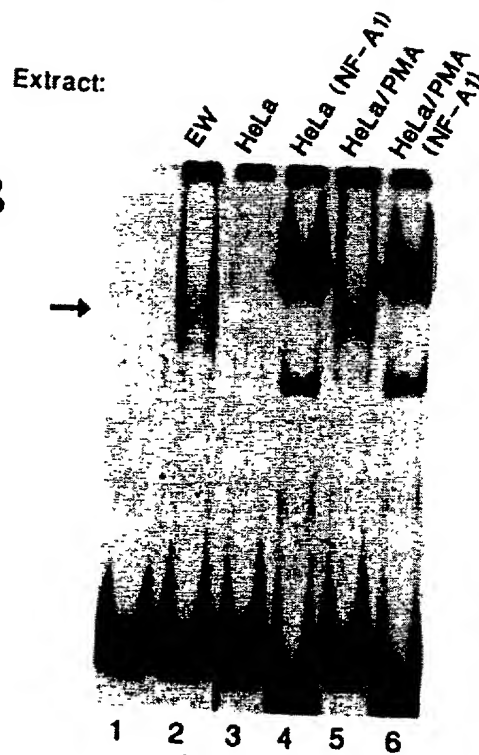
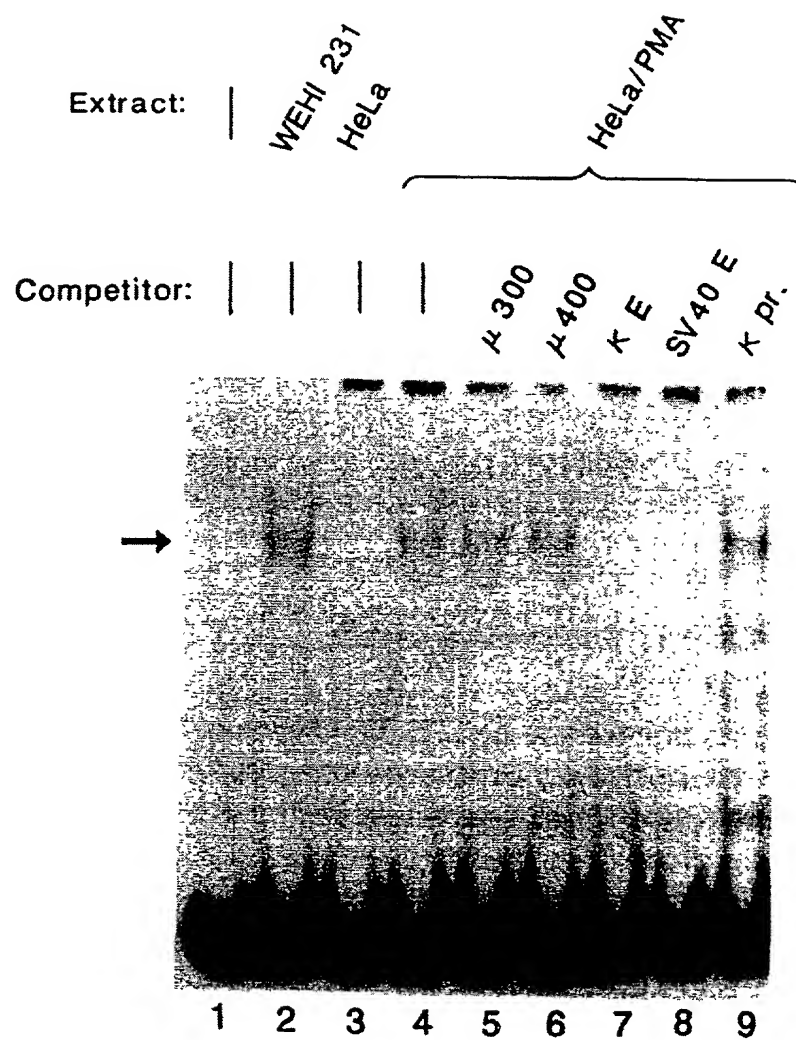


Figure 24C



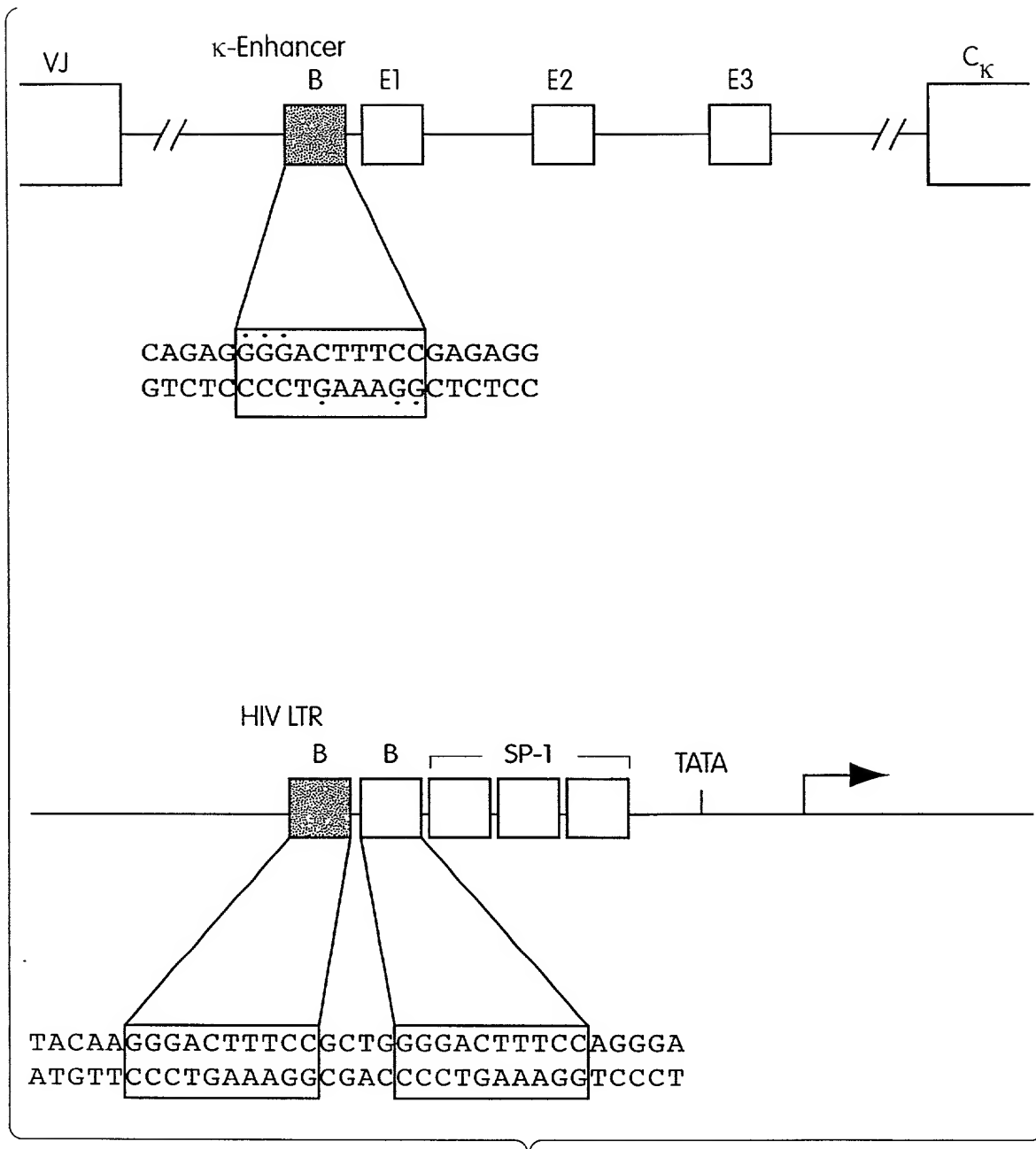


Fig. 25

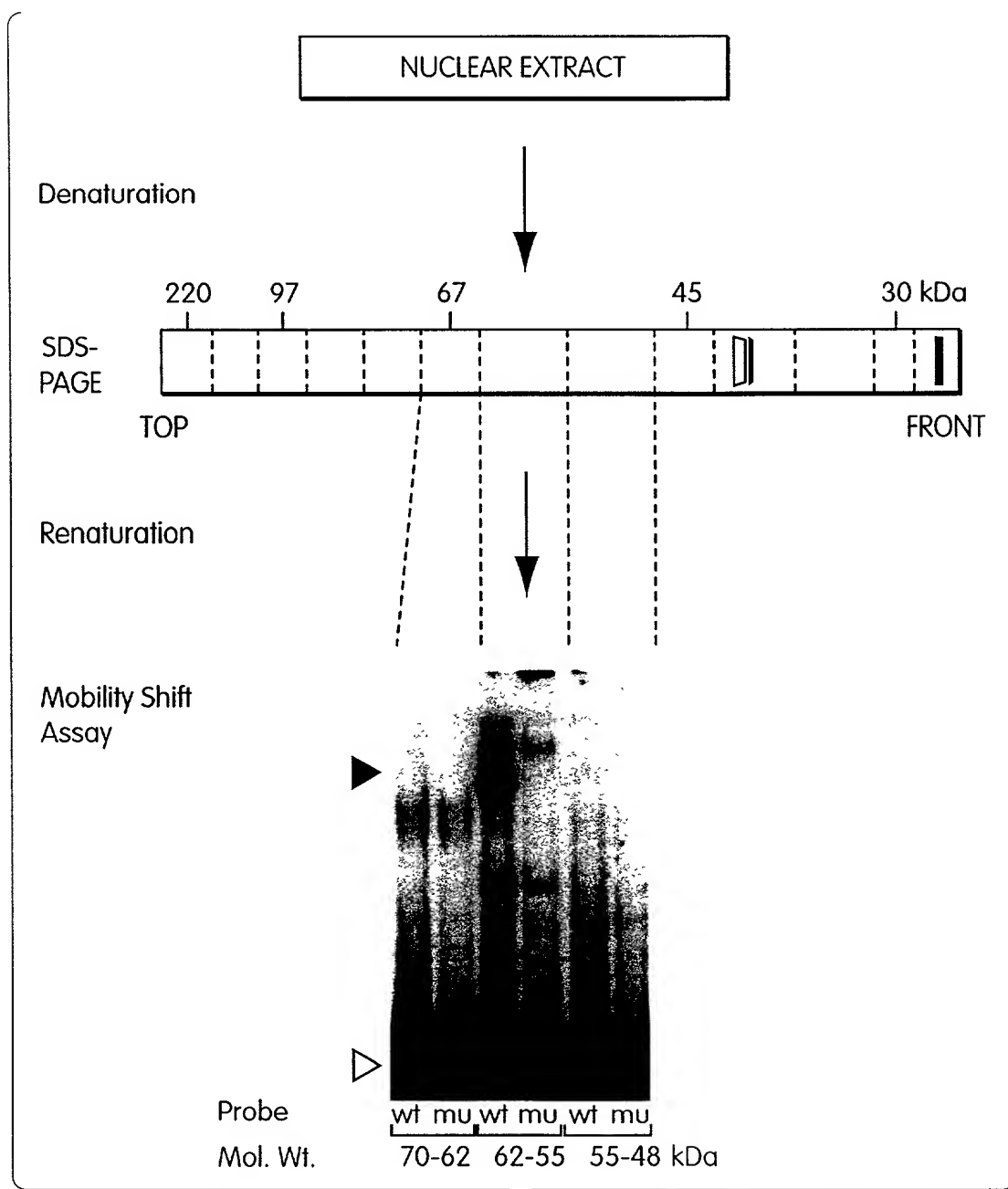


Fig. 26A

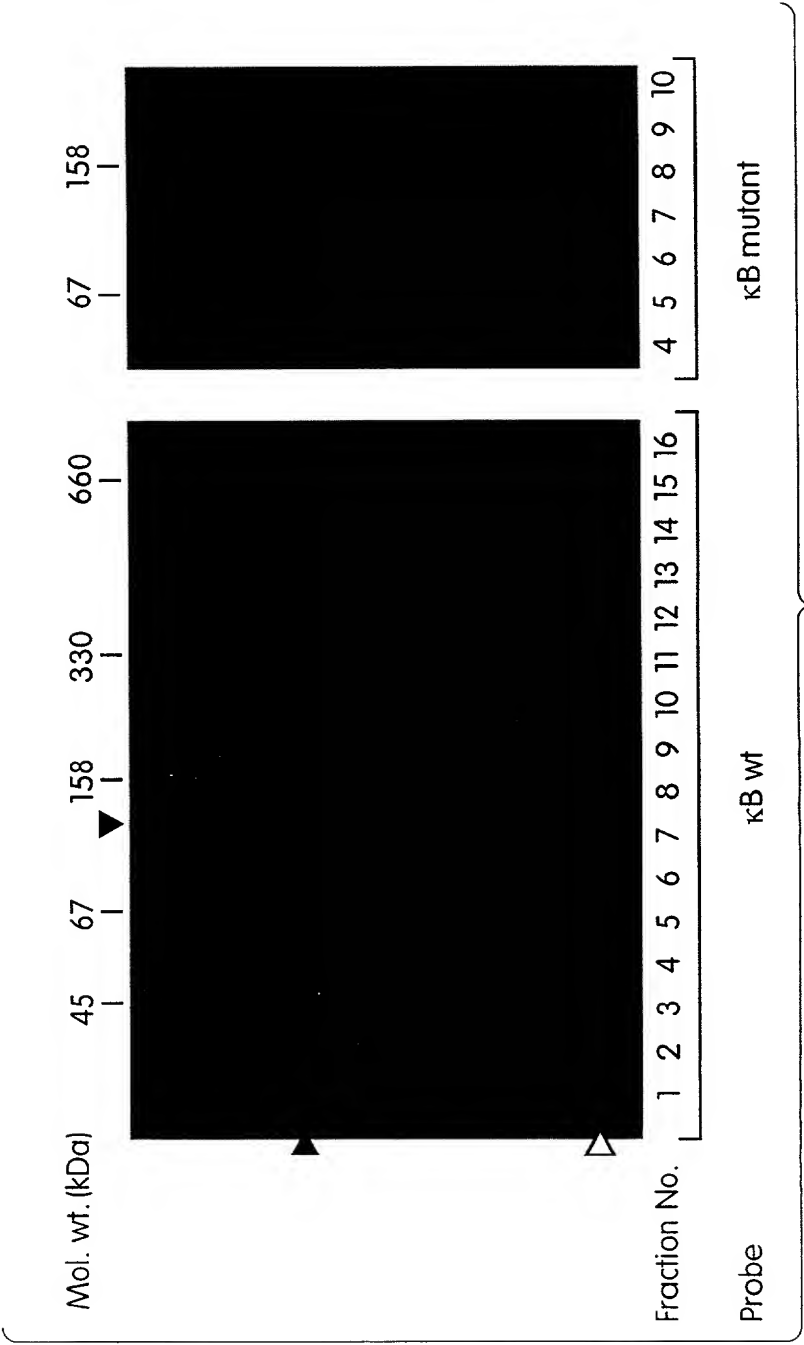


Fig. 26B

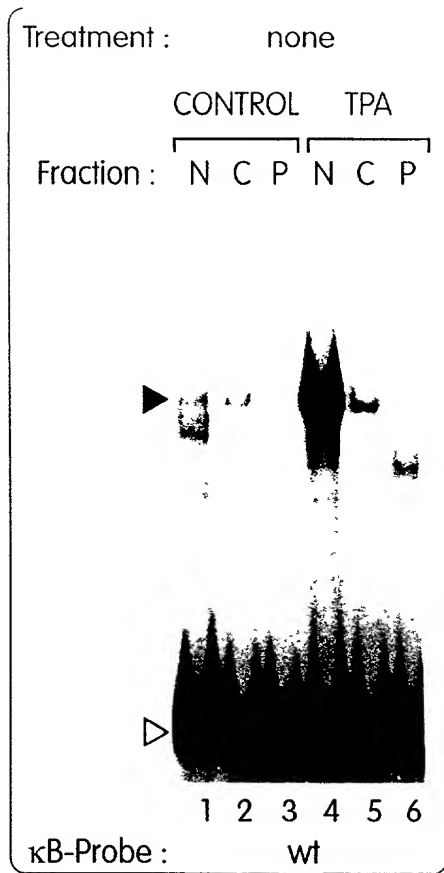


Fig. 27A

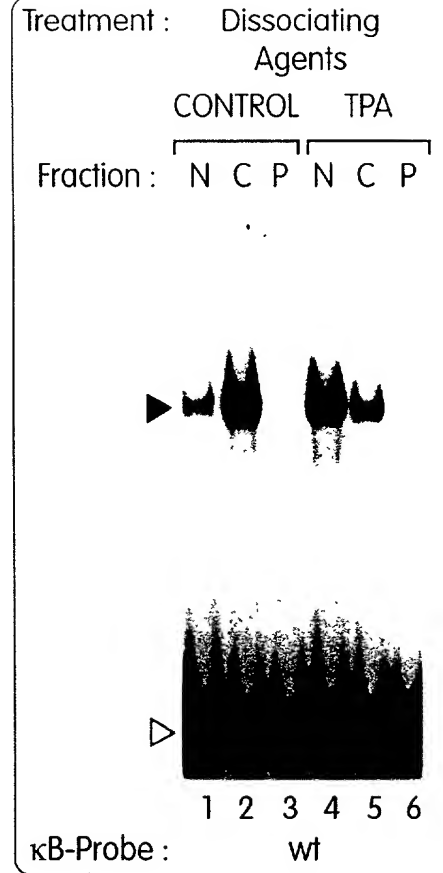


Fig. 27B

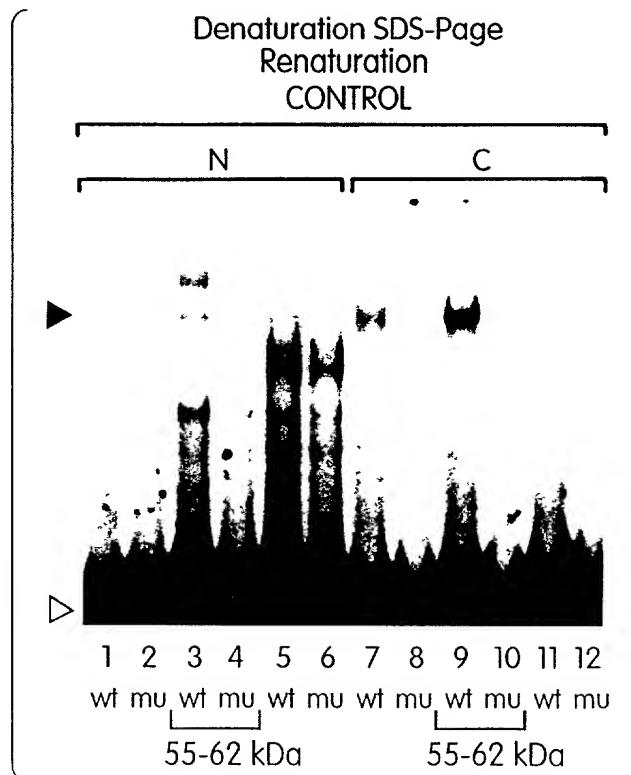


Fig. 27C

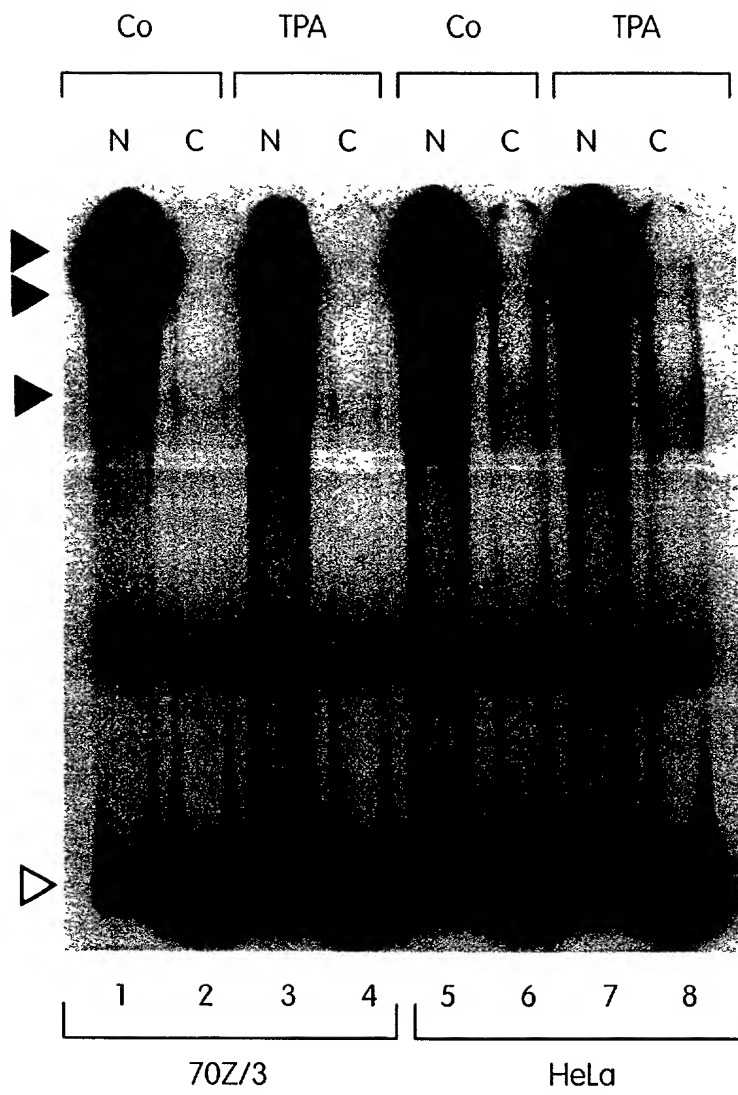


Fig. 28

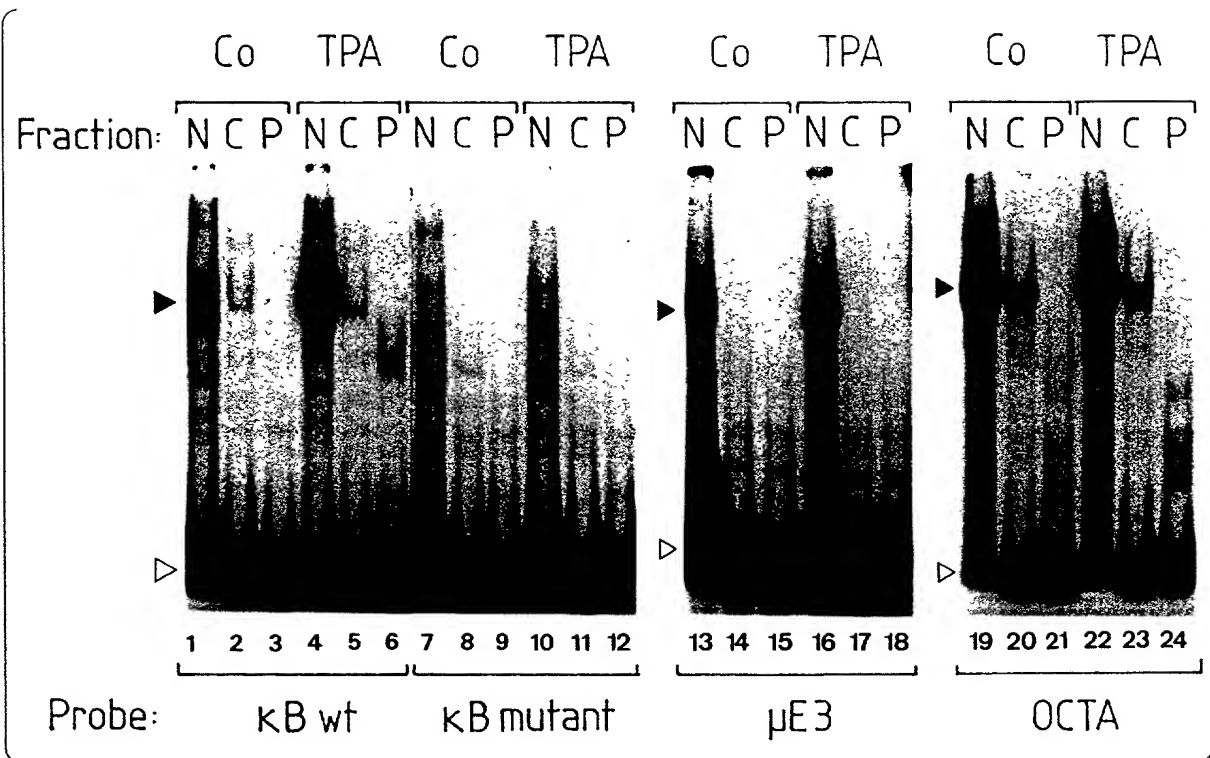


Fig. 29

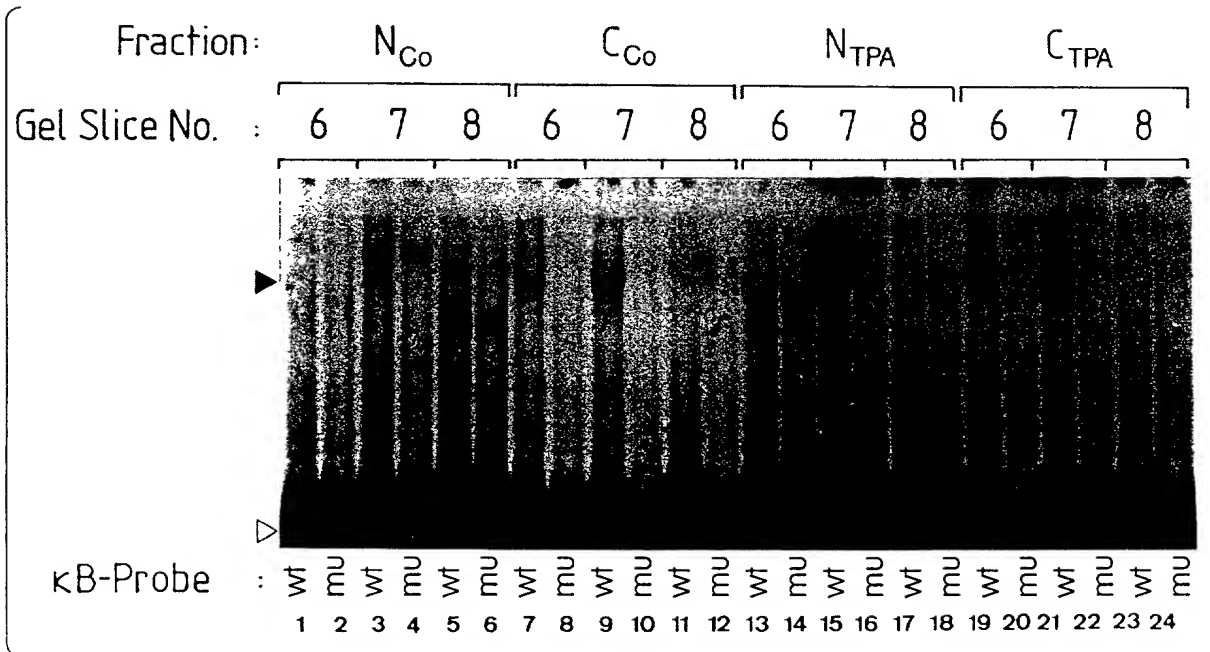
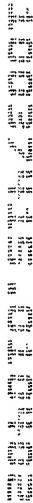
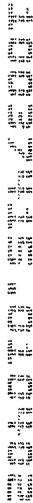


Fig. 30

[illegible][illegible]

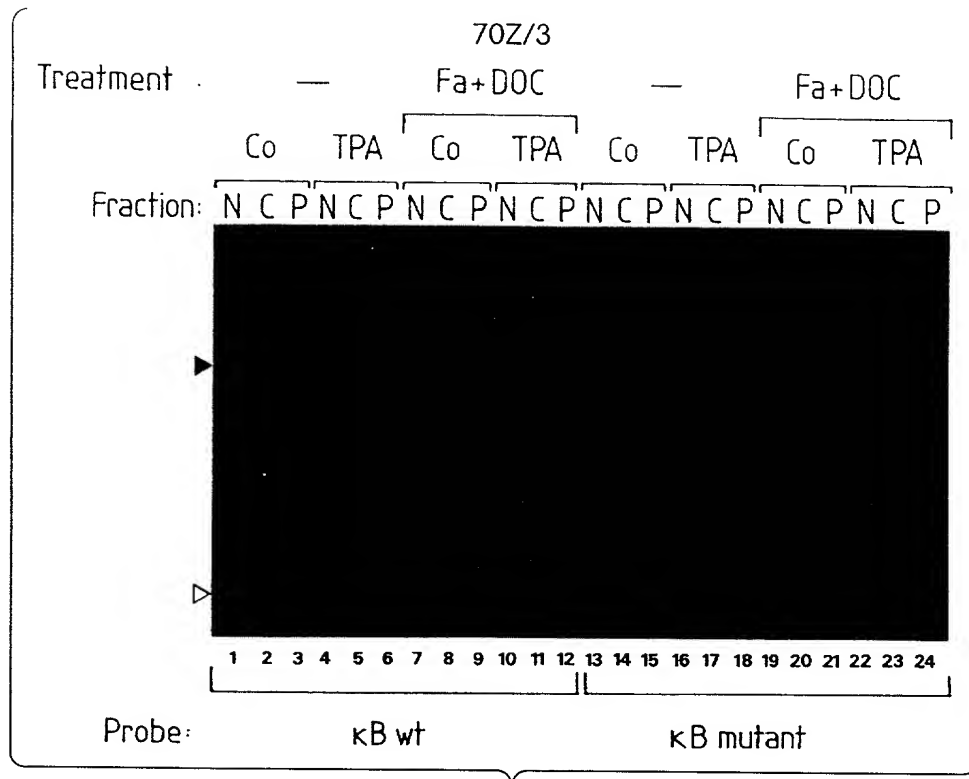


Fig. 32

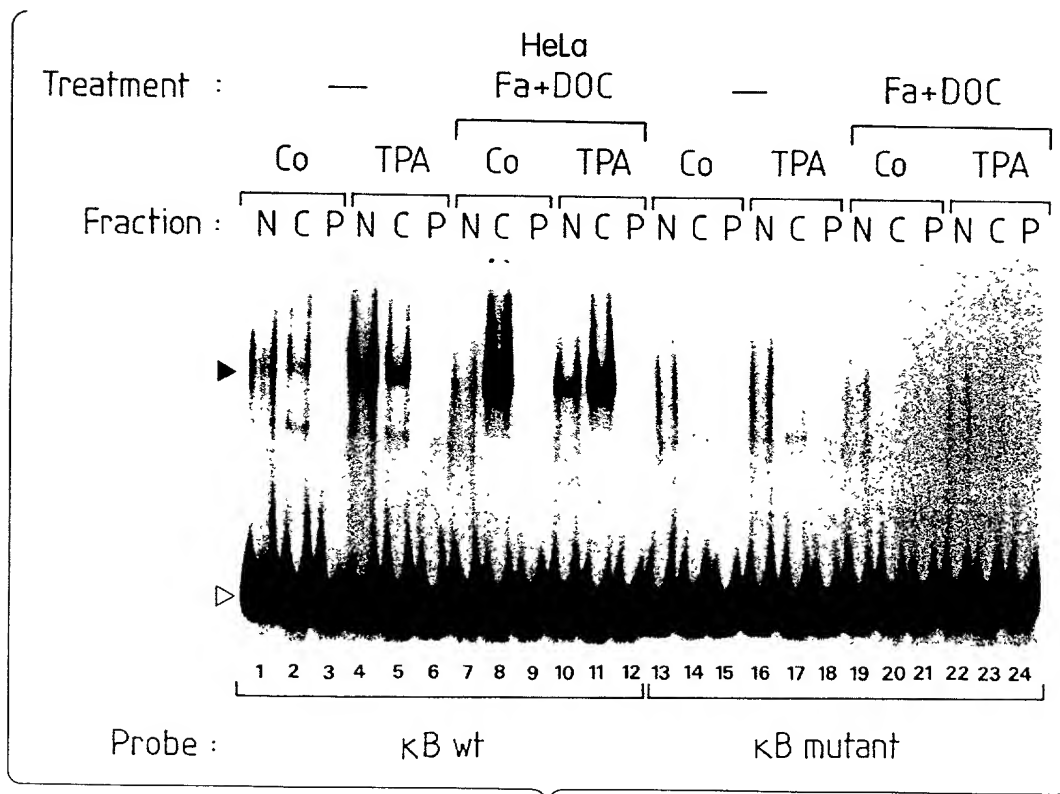


Fig. 33

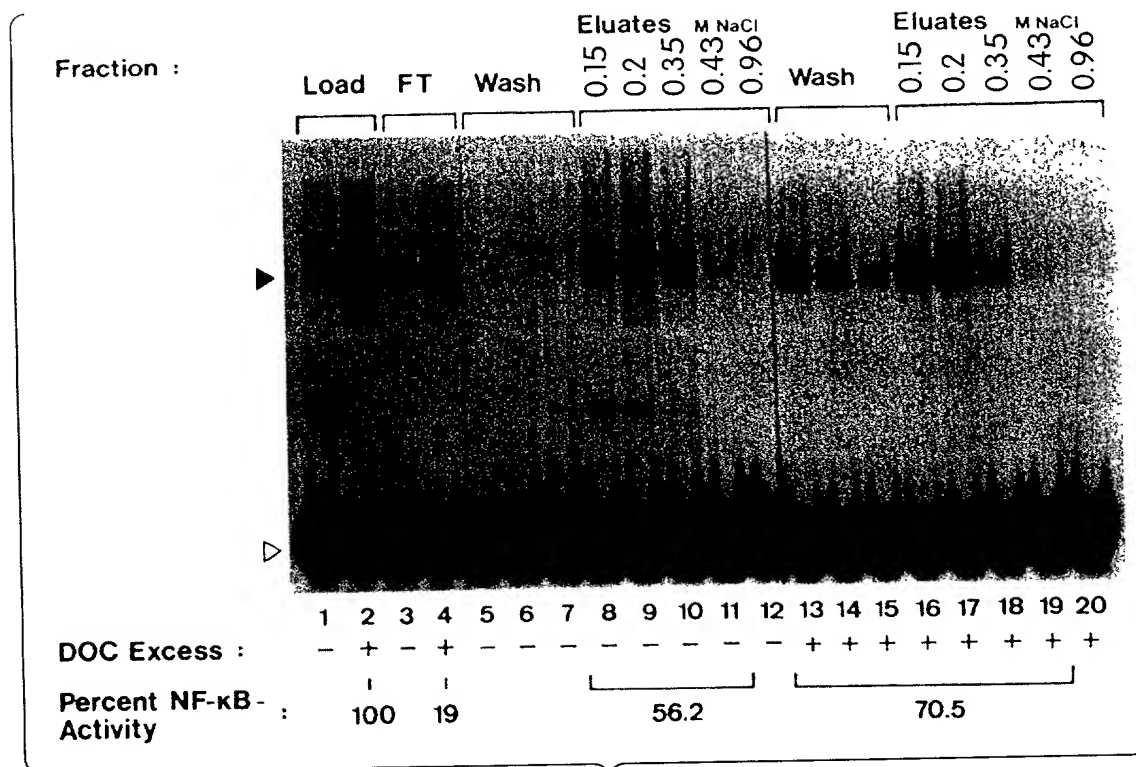


Fig. 34A

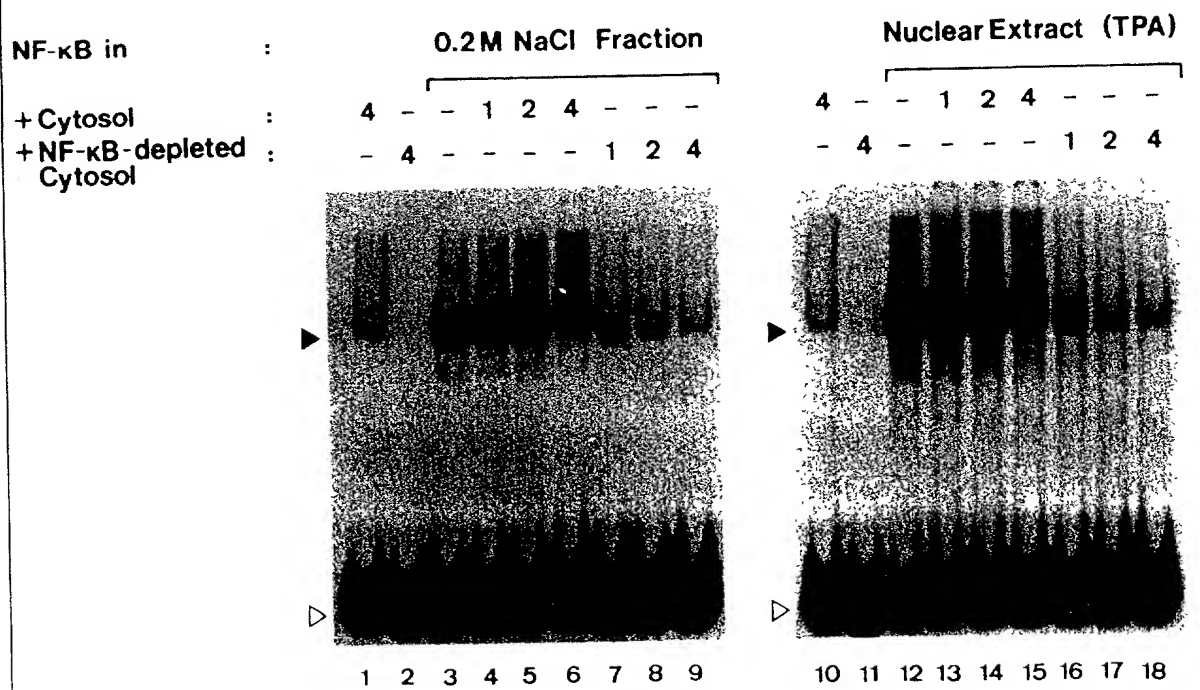


Fig. 34B

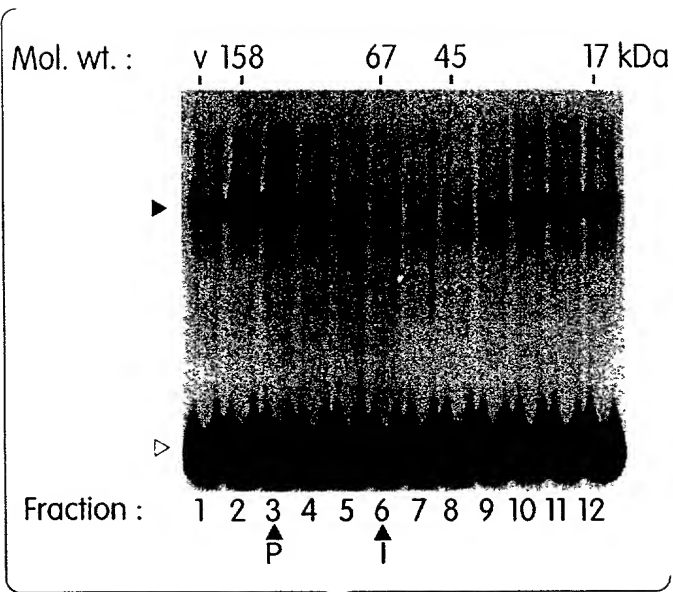


Fig. 35A

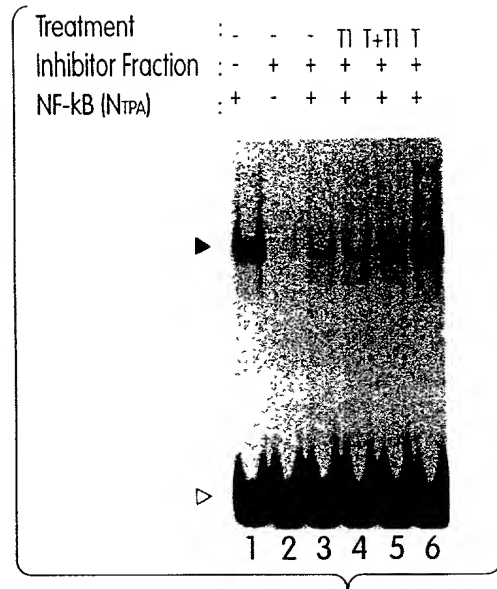


Fig. 35B

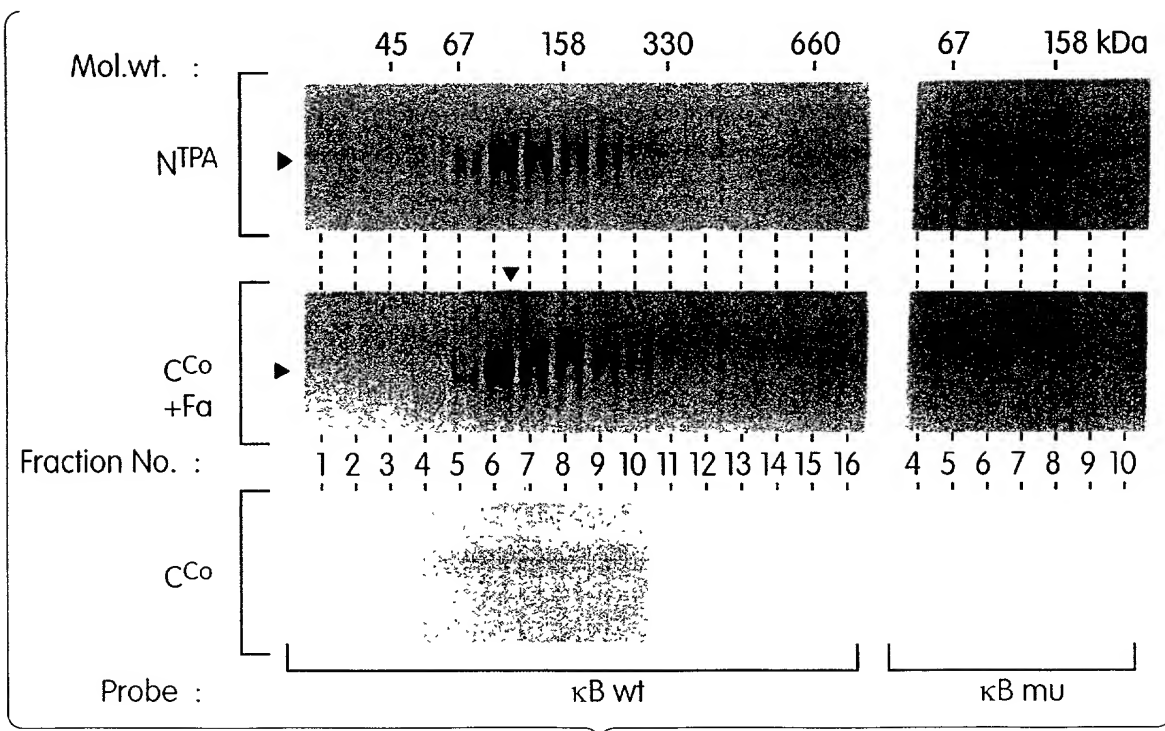


Fig. 35C

49/56

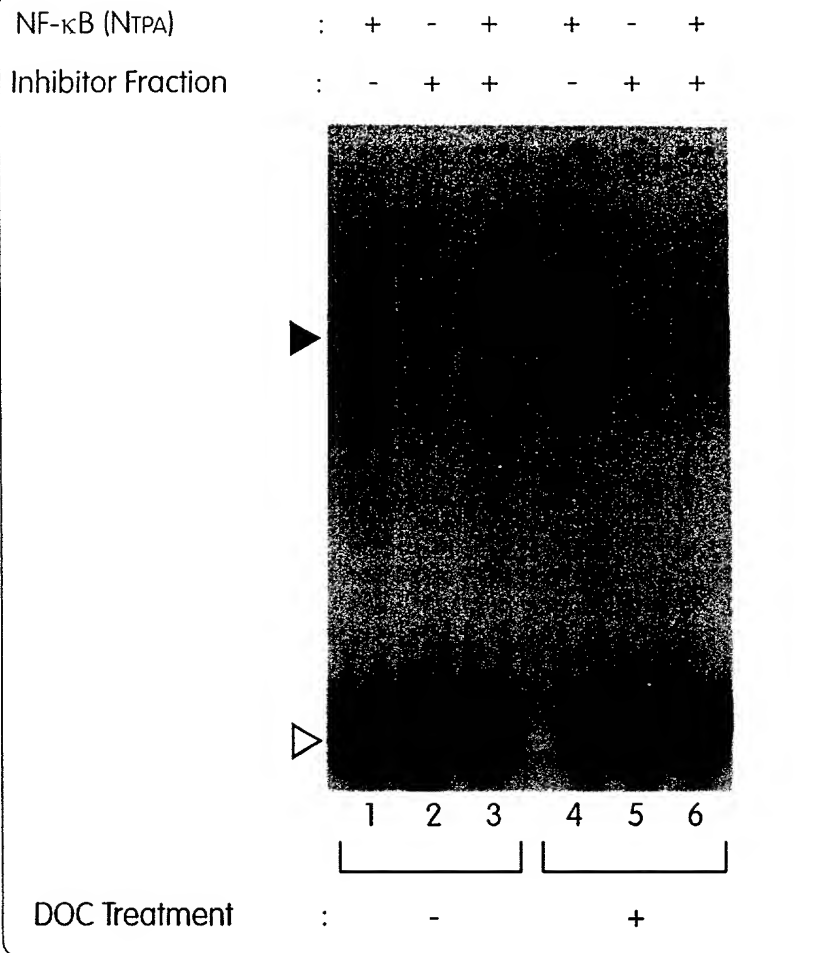


Fig. 36A

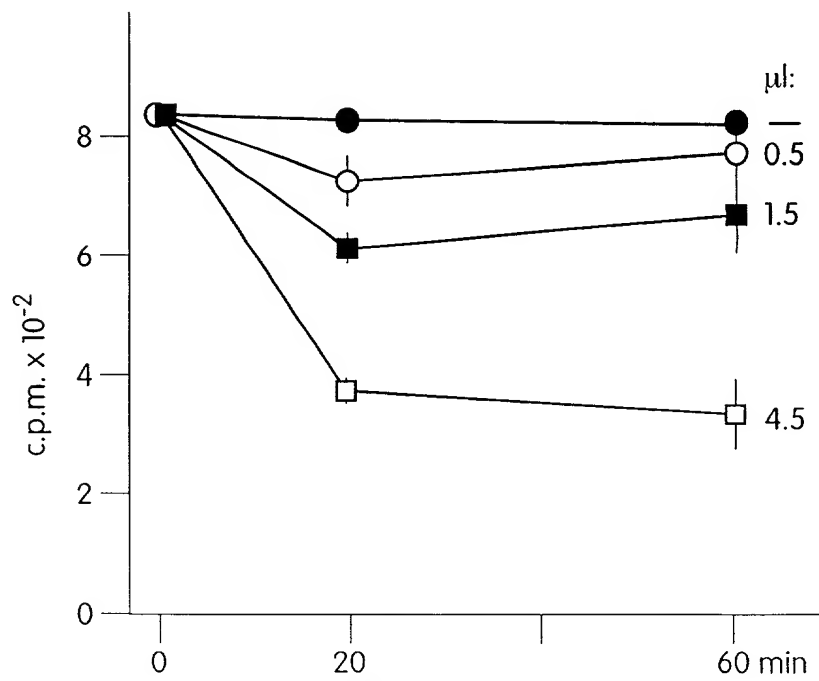


Fig. 36B

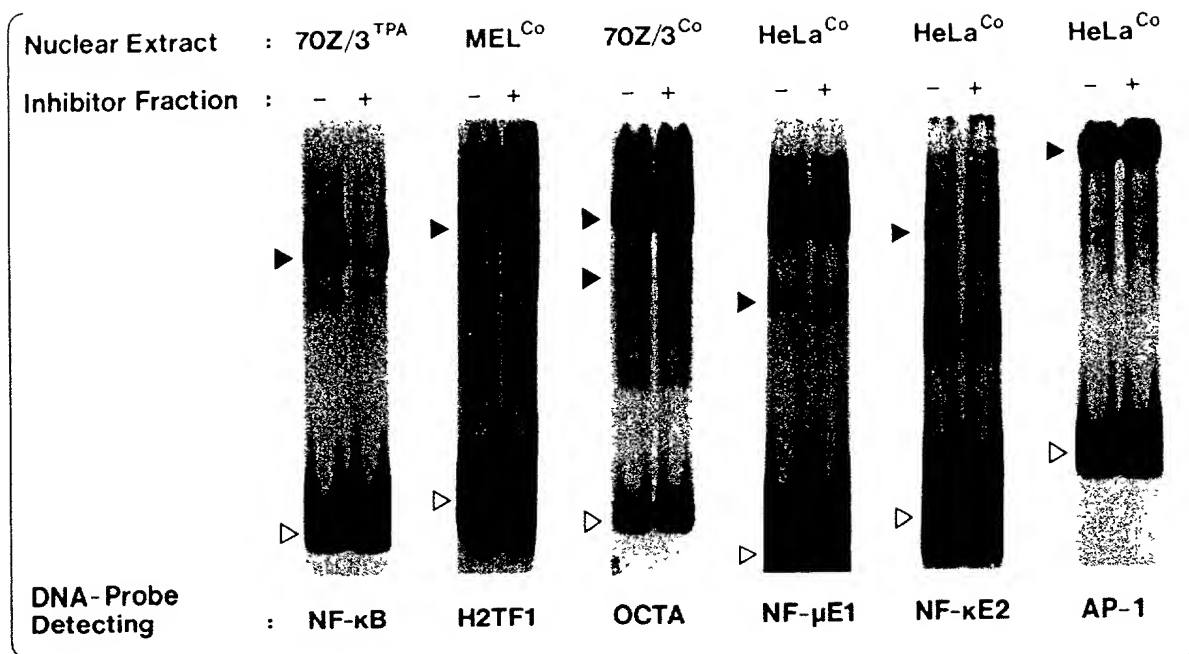


Fig. 37A

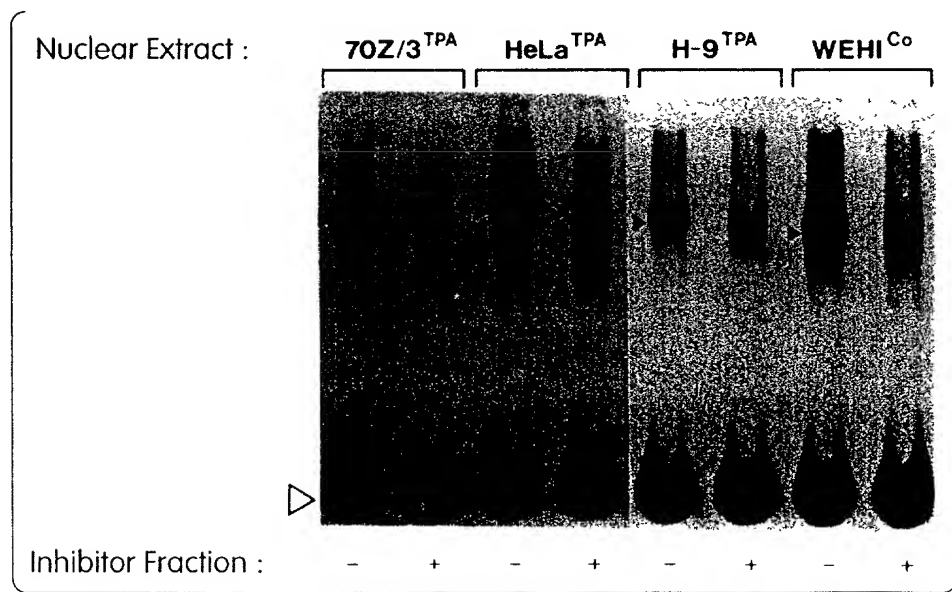


Fig. 37B

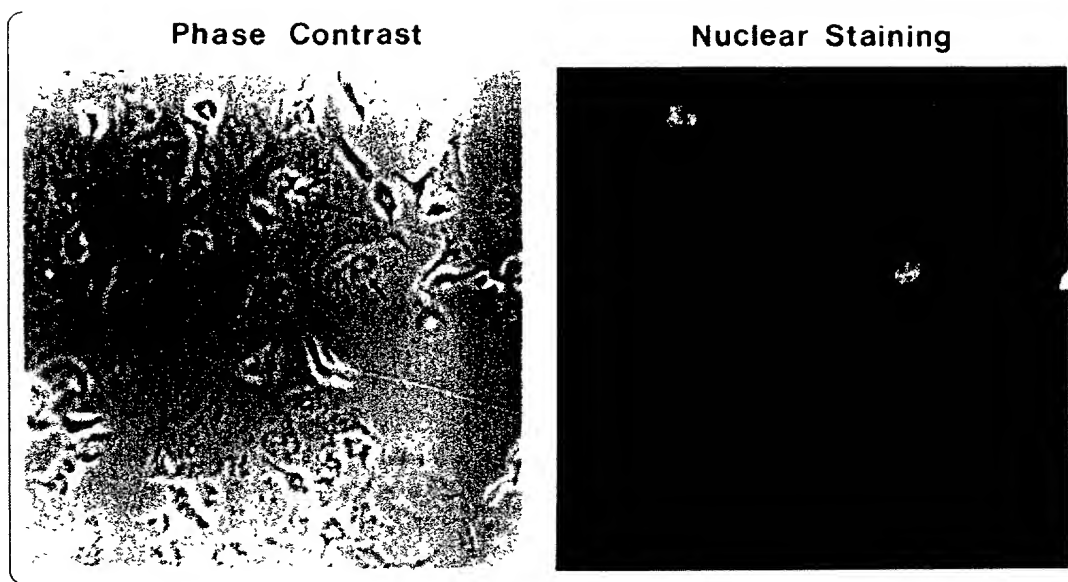


Fig. 38A

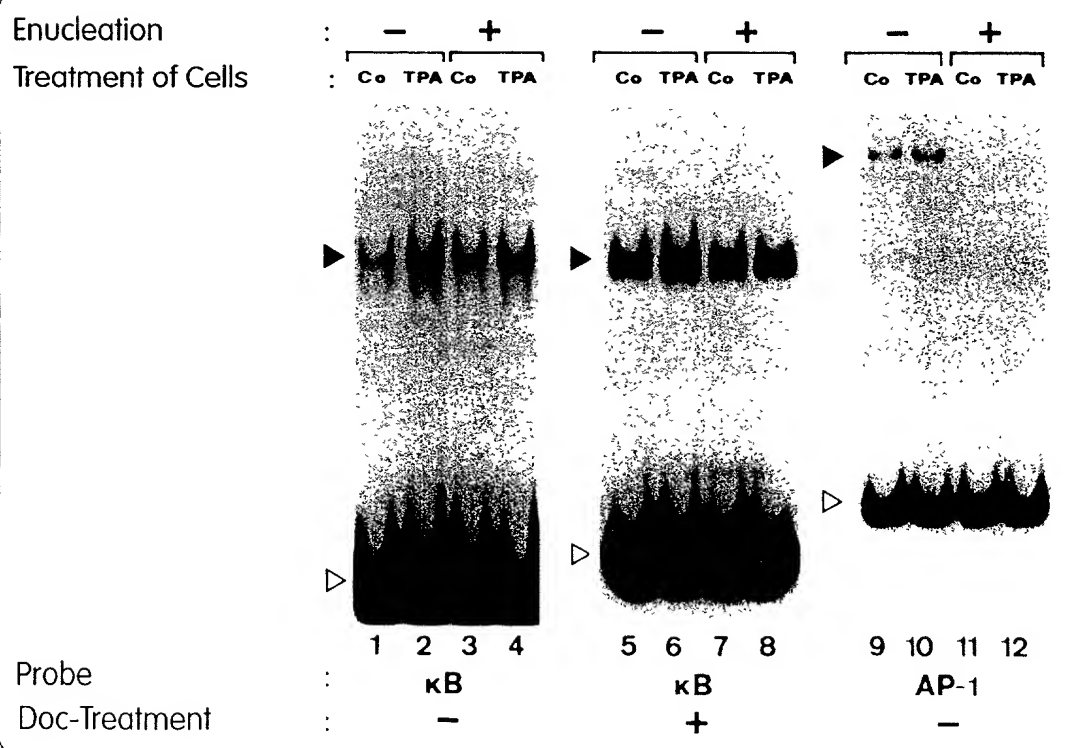


Fig. 38B

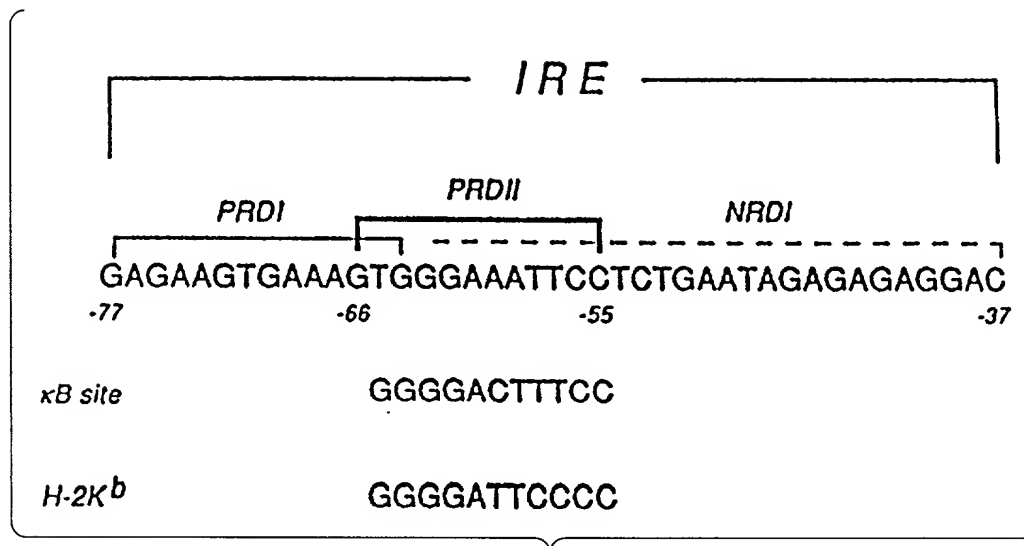
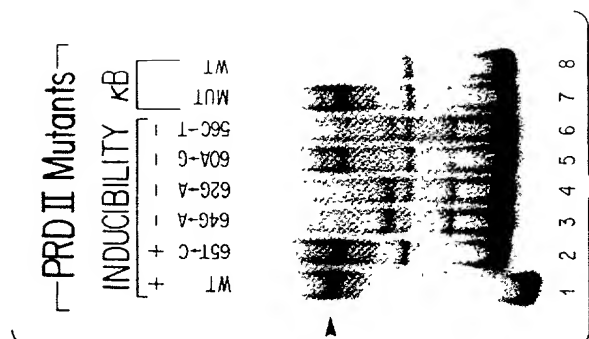
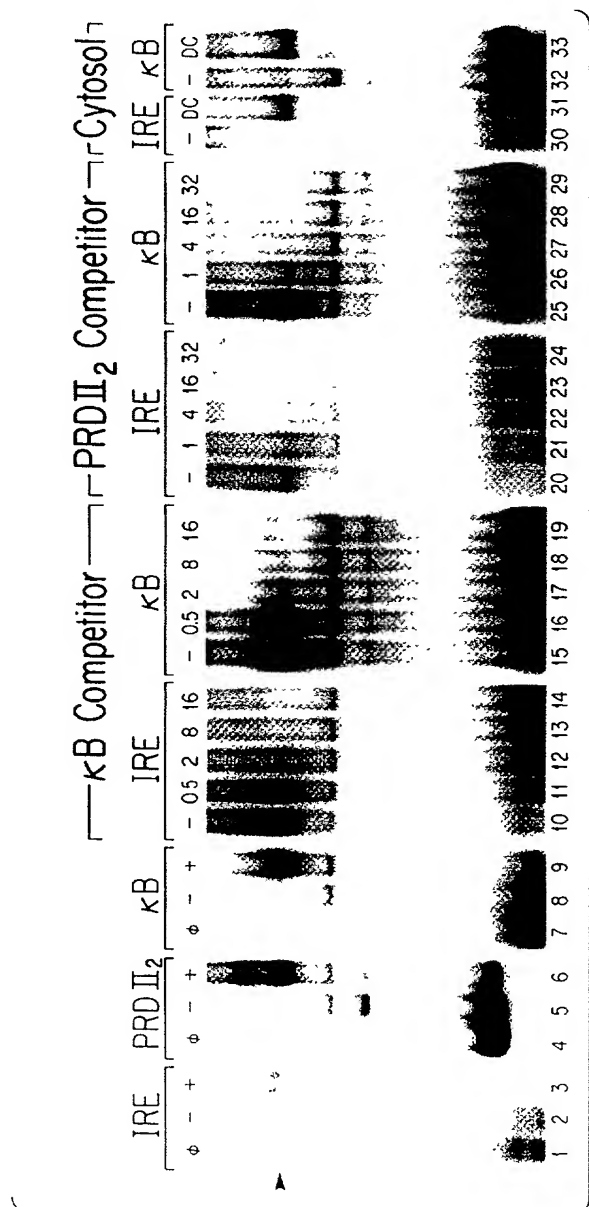


Fig. 39



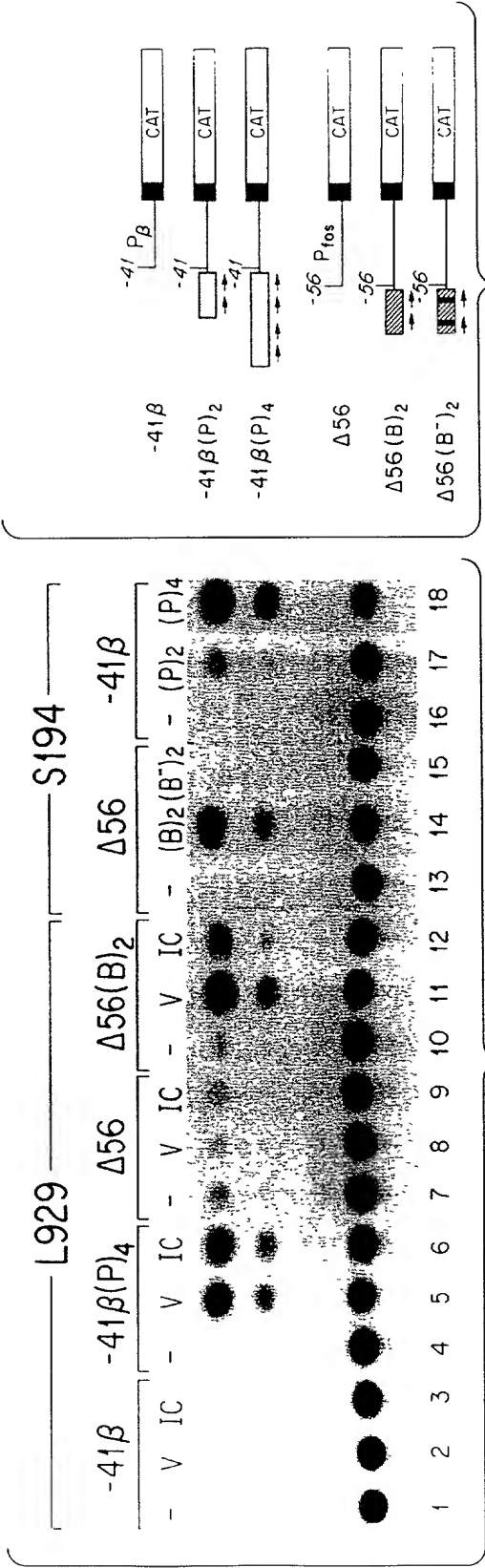


Fig. 41A

Fig. 41B

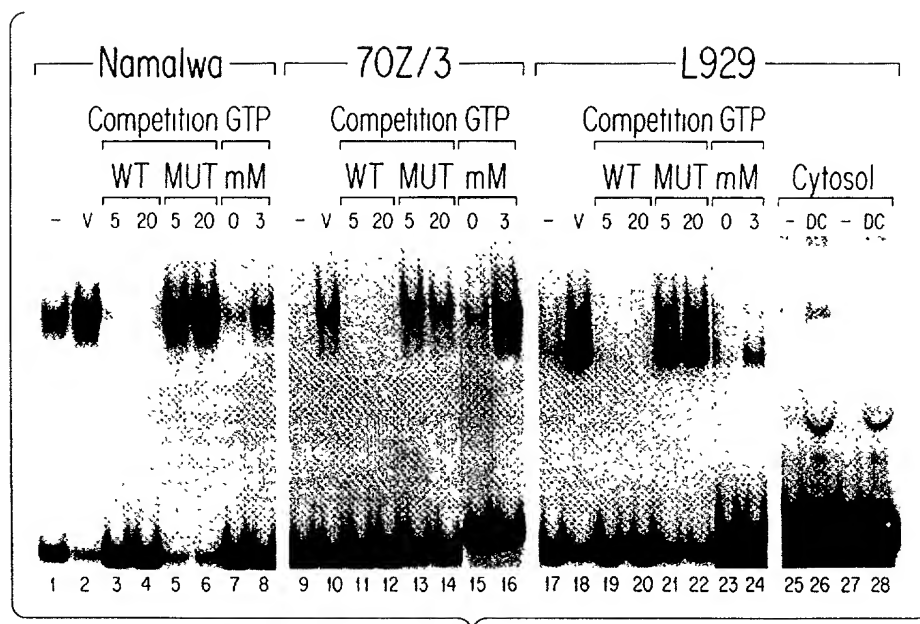


Fig. 42A

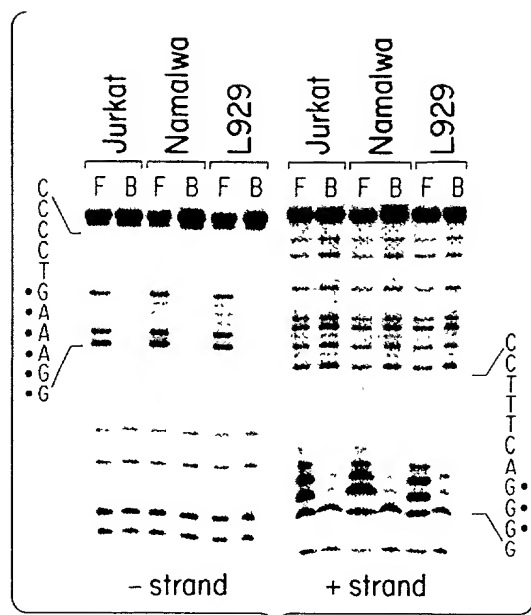


Fig. 42B

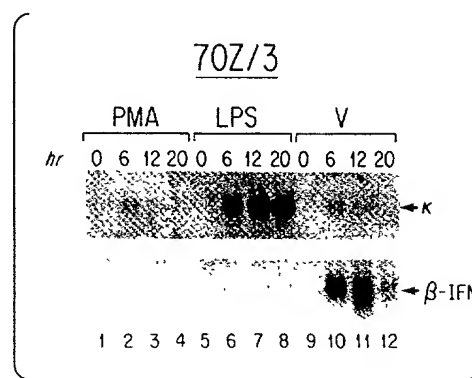


Fig. 42C

Figure 43 (continued)

GAGCCGCCCGCGTGGAGGGCTGCGAGCGCGCGCAAGGAACGGCAAGCGGGGCTGTGCCGCCCGACGACCGCC
E P P A V E G C E P P R K E R Q G G L L P P D D R H

ACGACAGCGGGCTGGACTCCATGAAGGAGGAGGAGTACAGGCAGCTGGTGGGGGAGCTGGAGGACATCCGCCCTGCA
D S G L D S M K E E Y R Q L V R E L E D I R L Q

GCCCCGAGCGCGCGCGCGCACGCCCTGGCGCCAGCAGCTCACCGAGGACGGCGACACTTTTCTCCACTTG
P R E P P A R P H A W A Q Q L T E D G D T F L H L

GCGATCATTCAGGAGGAAAGGCCCTGAGCCTGGAGGTGATCCGGCAGGCCGCTGGGACGCCGCTTCTGAACT
A I I H E E K A L S L E V I R Q A A G D A A F L N F

Ank. I
TCCAGAACAACCTCAGCCAGACTCCGCTCCACCTGGCGGTGATCACGGACCGCCGAAATCGCCGAGCACCTGCT
Q N N L S Q T P L H L A V I T D Q A E I A E H L L

Ank. II
GAAGGCTGGCTGCGACCTGGATGTCAGGGACTTCCGTGGGAACACCCCGCTCCACATCGCCTGCCAGCAGGGCTCG
K A G C D L D V R D F R G N T P L H I A C Q Q G S

Ank. III
CTCCGCAGCGTCAGTCTCACGCAGCACTGCCAGCCCCACCACTCCTCGCCGTCCTGCAGGCCCACTACA
L R S V S V L T Q H C Q P H H L L A V L Q A T N Y N

ACGGCCATACATGTCCTCATTTGGCATCTATTCAAGGATACCTGGCTGTTGTGGAATACCTGCTGCTCTTAGGAGC
G H T C L H L A S I Q G Y L A V V E Y L L S L G A

Ank. IV
AGATGTAATGCTCAGGAGCCATGCAATGGGAGAACAGCACTACACTTGGCCGTAGACCTTCAGAACTCAGACCTG
D V N A Q E P C N G R T A L H L A V D L Q N S D L

Ank. V

Figure 43 (continued)

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GTGTCACTTCTGGTGAAACACGGGCCAGATGTGAACAAAGTGACCTACCAGGGCTACTCCCCATACCAGCTTACAT
V S L L V K H G P D V N K V T Y Q G Y S P Y Q L T W
GGCAGAGACAACGCCAGCATACAGGAGCAGCTGAAGCTGCTGACCACAGCTGACCTGCAGATACTGCCCGAAAGT
A E T T P A Y R S S 354
GAGGATGAGGAGAGCAGTGAATCAGAGCCAGAGTTCACAGAGGATGAACCTTATGTATGATGACTGCTGTATTGGAG
GAAGACAGCTGACATTTTAAAGCAGAGGTTTCTGTGAGAAAGTGACTGTGTACATAATGTATAGGAAAAAAGCCTGA
CTTTCCTTCATTTAAAAAGAAAGTCTATCTCGAAGGAGAAAAAAGTACTGAGATACTACACTGCCCAGCCAGGAGC
ACATCATGCTAACAGGTTCCATGCTCTGACCTGTACTTAAGTAACGGGATGGGATGTGTAACATCGTTAAGAGATC
AGTGAACATGCACACCATCTGATAAAGAGCCACGTTATCTAATTTCTCTGCCACATGAGGATAACGGACTGCACGT
CCAATGTGCTGTTGTCAGAAATGCGTTTGAGAGCTGCCCTTGAGACACTAAGTCTGTGAGGAGTGCTCATCCCCCT
CGGTGGCAAGACAGGCTTGCACAAACGTCCTCATCTGCTTGAAGACTGTGAGGTTGGCATTAGGTTGAGGCACCTGCT
GTGCCCCTGCTCCCTGACCCCTGGCTGCTCAGGGTTGAGGAGTCCGACCATGGGAGAGGTGACCTGGCTGCTGGGAGG
AAGGTAGCAATGATGTAACTGTGGGCATTTGGAAACTGTGTGTTTACACACCATGTGTGTCTATAAATTGCTACACTT
TTTAGCAACTGTATAGAATGTAAATACTGTACATCTTTGTTTATAATTATTTTGGTACCTGTGAGATATGTATTTA
TTAAAAAAGGCAGATTTCTGTAAAAA

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